encoded protein. AT340_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AT340_1 protein").

The partial nucleotide sequence of AT340_1, including its 3' end and a poly(A) tail, as presently determined is reported in SEQ ID NO:114. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:115. The predicted amino acid sequence of the AT340_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:115. Amino acids 12 to 24 of SEQ ID NO:115 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 25. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the AT340_1 protein. Additional nucleotide sequence from the 5' portion of AT340_1 is reported in SEQ ID NO:113.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AT340_1 should be approximately 1100 bp.

The nucleotide sequence disclosed herein for AT340_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. AT340_1 demonstrated at least some similarity with sequences identified as AA039343 (zk39g04.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 485238 3'), R68951 (yi43g06.r1 Homo sapiens cDNA clone 142042 5' similar to SP:C35D10.1 CE01190), R77532 (yi76c01.r1 Homo sapiens cDNA), R92619 (yq04a04.r1 Homo sapiens cDNA clone 195918 5' similar to SP:C35D10.1 CE01190), and W60997 (zc99f09.s1 Pancreatic Islet Homo sapiens cDNA clone 339305 3'). The predicted amino acid sequence disclosed herein for AT340_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted AT340_1 protein demonstrated at least some similarity to sequences identified as U21324 (similar to S. cerevisiae hypothetical protein YKL166 [Caenorhabditis elegans]). Based upon sequence similarity, AT340_1 proteins and each similar protein or peptide may share at least some activity.

Clone "BG132_1"

A polynucleotide of the present invention has been identified as clone "BG132_1". BG132_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BG132_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BG132_1 protein").

The nucleotide sequence of the 5' portion of BG132_1 as presently determined is reported in SEQ ID NO:116. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:117. The predicted amino acid sequence of the BG132_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:117. Amino acids 121 to 133 of SEQ ID NO:117 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 134. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the BG132_1 protein. Additional nucleotide sequence from the 3' portion of BG132_1, including a poly(A) tail, is reported in SEQ ID NO:118.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BG132_1 should be approximately 2000 bp.

The nucleotide sequence disclosed herein for BG132_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BG132_1 demonstrated at least some similarity with sequences identified as AA078587 (7P05H12 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P05H12), H14301 (ym63c04.r1 Homo sapiens cDNA clone 163590 5' similar to gb:U03642_cds1 PROBABLE G PROTEIN-COUPLED RECEPTOR APJ (HUMAN)), L09249 (putative G-protein coupled receptor, rhodopsin family), S79811 (adrenomedullin receptor [rats, lung, mRNA]), T36034 (rchd523 gene differentially expressed in cardiovascular disease), U58828 (Human IL8-related receptor (DRY12) mRNA, complete cds), and Y08162 (H.sapiens mRNA for heptahelix receptor). The predicted amino acid sequence disclosed herein for BG132_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BG132_1 protein demonstrated at least some similarity to sequences identified as L06109 (G protein-coupled receptor [Gallus gallus]), L34339 (galanin receptor [Homo sapiens]), U30290 (galanin receptor GALR1 [Rattus norvegicus]), U58828 (IL8-related receptor [Homo sapiens]), W03739 (rchd523 gene product (G protein-coupled receptor)), X98510 (G protein-coupled receptor [Homo sapiens]), and Y08162 (heptahelix receptor [Homo sapiens]). Based upon sequence similarity, BG132_1 proteins and each similar protein or peptide may share at least some activity.

Clone "BG219_2"

A polynucleotide of the present invention has been identified as clone "BG219_2". BG219_2 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding

a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BG219_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BG219_2 protein").

The nucleotide sequence of BG219_2 as presently determined is reported in SEQ ID NO:119, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BG219_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:120.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BG219_2 should be approximately 700 bp.

The nucleotide sequence disclosed herein for BG219_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BG219_2 demonstrated at least some similarity with sequences identified as AA210695 (zr88b05.s1 Soares NbHTGBC Homo sapiens cDNA clone 682737 3'), C01459 (HUMGS0008450, Human Gene Signature, 3'-directed cDNA sequence), N22628 (EST49p115 Homo sapiens cDNA clone 49p115), and T26211 (Human gene signature HUMGS08450). Based upon sequence similarity, BG219_2 proteins and each similar protein or peptide may share at least some activity.

Clone "BG366_2"

A polynucleotide of the present invention has been identified as clone "BG366_2". BG366_2 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BG366_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BG366_2 protein").

The nucleotide sequence of BG366_2 as presently determined is reported in SEQ ID NO:121, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BG366_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:122. The amino acid sequence of another protein that could be encoded by BG366_2 is reported in SEQ ID NO:283.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BG366_2 should be approximately 3000 bp.

The nucleotide sequence disclosed herein for BG366_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BG366_2 demonstrated at least some similarity with sequences identified as N39453

(yy49h03.s1 Homo sapiens cDNA clone 276917 3'). Based upon sequence similarity, BG366_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the BG366_2 protein sequence centered around amino acid 92 of SEQ ID NO:122.

Clone "BV172_2"

A polynucleotide of the present invention has been identified as clone "BV172_2". BV172_2 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BV172_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BV172_2 protein").

The nucleotide sequence of BV172_2 as presently determined is reported in SEQ ID NO:123, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BV172_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:124.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BV172_2 should be approximately 1650 bp.

The nucleotide sequence disclosed herein for BV172_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BV172_2 demonstrated at least some similarity with sequences identified as No significant hits were found in the database. The TopPredII computer program predicts a potential transmembrane domain within the BV172_2 protein sequence centered around amino acid 19 of SEQ ID NO:124. The nucleotide sequence of BV172_2 indicates that it may contain one or more of the following types of repetitive elements: an element similar to chicken CR1, human L1, Mer33.

Clone "CC247_10"

A polynucleotide of the present invention has been identified as clone "CC247_10". CC247_10 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino

acid sequence of the encoded protein. CC247_10 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CC247_10 protein").

The nucleotide sequence of CC247_10 as presently determined is reported in SEQ ID NO:125, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CC247_10 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:126. Amino acids 1 to 8 of SEQ ID NO:126 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 9. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CC247_10 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CC247_10 should be approximately 550 bp.

The nucleotide sequence disclosed herein for CC247_10 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CC247_10 demonstrated at least some similarity with sequences identified as AA291226 (zs47d03.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone 700613 5'), T05738 (EST03627 Homo sapiens cDNA clone HFBDF64), W51195 (ma14b04.r1 Life Tech mouse brain Mus musculus cDNA clone 304495 5'), and W93640 (zd95d09.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 357233 3'). The predicted amino acid sequence disclosed herein for CC247_10 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CC247_10 protein demonstrated at least some similarity to sequences identified as M62424 (thrombin receptor [Homo sapiens]). The predicted CC247_10 protein is highly hydrophobic. Based upon sequence similarity, CC247_10 proteins and each similar protein or peptide may share at least some activity.

Clone "CI480_9"

A polynucleotide of the present invention has been identified as clone "CI480_9". CI480_9 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CI480_9 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CI480_9 protein").

The nucleotide sequence of CI480_9 as presently determined is reported in SEQ ID NO:127, and includes a poly(A) tail. What applicants presently believe to be the proper reading

frame and the predicted amino acid sequence of the CI480_9 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:128. Amino acids 39 to 51 of SEQ ID NO:128 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 52. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CI480_9 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CI480_9 should be approximately 1940 bp.

The nucleotide sequence disclosed herein for CI480_9 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CI480_9 demonstrated at least some similarity with sequences identified as N99342 (IMAGE:20093 Homo sapiens cDNA clone 20093), R89725 (ym99d09.r1 Homo sapiens cDNA clone 167057 5'), and U60644 (Human HU-K4 mRNA, complete cds). The predicted amino acid sequence disclosed herein for CI480_9 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CI480_9 protein demonstrated at least some similarity to sequences identified as U60644 (HU-K4 [Homo sapiens]). Based upon sequence similarity, CI480_9 proteins and each similar protein or peptide may share at least some activity.

CI480_9 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 63 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "CO722_1"

A polynucleotide of the present invention has been identified as clone "CO722_1". CO722_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CO722_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CO722_1 protein").

The nucleotide sequence of CO722_1 as presently determined is reported in SEQ ID NO:129, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CO722_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:130. Amino acids 17 to 29 of SEQ ID NO:130 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 30. Due to the hydrophobic nature of the predicted leader/signal

sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CO722_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CO722_1 should be approximately 6800 bp.

The nucleotide sequence disclosed herein for CO722_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CO722_1 demonstrated at least some similarity with sequences identified as AA186616 (zp71a08.s1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone 625622 3' similar to contains Alu repetitive element), H10376 (ym08a03.s1 Homo sapiens cDNA clone 47067 3'), N86013 (J5997F Fetal heart, Lambda ZAP Express Homo sapiens cDNA), U55258 (Human hBRAVO/Nr-CAM precursor (hBRAVO/ Nr-CAM) gene, complete cds), W19770 (zb39d01.r1 Soares parathyroid tumor NbHPA Homo sapiens), W31608 (zb91d09.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone), and X58482 (Chicken mRNA for neuronal transmembrane protein Nr-CAM, ng-CAM related). The predicted amino acid sequence disclosed herein for CO722_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CO722_1 protein demonstrated at least some similarity to sequences identified as AB002341 (KIAA0343 [Homo sapiens]) and X58482 (Nr-CAM protein [Gallus gallus]). Based upon sequence similarity, CO722_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the CO722_1 protein sequence, centered around amino acids 610 and 1070 of SEQ ID NO:130, respectively.

CO722_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 160 kDa was detected in conditioned media fractions using SDS polyacrylamide gel electrophoresis.

Clone "CT748_2"

A polynucleotide of the present invention has been identified as clone "CT748_2". CT748_2 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CT748_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CT748_2 protein").

The nucleotide sequence of CT748_2 as presently determined is reported in SEQ ID NO:131, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CT748_2 protein corresponding to the

foregoing nucleotide sequence is reported in SEQ ID NO:132. Amino acids 281 to 293 of SEQ ID NO:132 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 294. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CT748_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CT748_2 should be approximately 5500 bp.

The nucleotide sequence disclosed herein for CT748_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CT748_2 demonstrated at least some similarity with sequences identified as T48063 (yb24f03.s1 Homo sapiens cDNA clone 72125 3') and X54175 (Human specific Alu element (HS C4N2) DNA). The predicted amino acid sequence disclosed herein for CT748_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CT748_2 protein demonstrated at least some similarity to sequences identified as Z36714 (cyclin F [Homo sapiens]). Based upon sequence similarity, CT748_2 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of CT748_2 indicates that it may contain an Alu repetitive element.

Clone "AJ1_1"

A polynucleotide of the present invention has been identified as clone "AJ1_1". AJ1_1 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. AJ1_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AJ1_1 protein").

The nucleotide sequence of the 5' portion of AJ1_1 as presently determined is reported in SEQ ID NO:133. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:134. The predicted amino acid sequence of the AJ1_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:134. Additional nucleotide sequence from the 3' portion of AJ1_1, including a poly(A) tail, is reported in SEQ ID NO:135.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AJ1_1 should be approximately 925 bp.

The predicted amino acid sequence disclosed herein for AJ1_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The

predicted AJ1_1 protein demonstrated at least some similarity to sequences identified as U39060 (GRIP1 [Mus musculus]). Based upon sequence similarity, AJ1_1 proteins and each similar protein or peptide may share at least some activity.

Clone "AQ73_3"

A polynucleotide of the present invention has been identified as clone "AQ73_3". AQ73_3 was isolated from a human adult ovary (PA-1 teratocarcinoma, untreated tissue pooled with retinoic-acid-treated and activin-treated tissue) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. AQ73_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AQ73_3 protein").

The nucleotide sequence of AQ73_3 as presently determined is reported in SEQ ID NO:136, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the AQ73_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:137.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AQ73_3 should be approximately 2800 bp.

The nucleotide sequence disclosed herein for AQ73_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. AQ73_3 demonstrated at least some similarity with sequences identified as AA514474 (nf57g01.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone 924048), T47520 (Human hepatoma-derived growth factor (HDGF-2) cDNA), W24708 (zb62e08.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 308198 5'), and W45513 (zc27g08.s1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 323582 3'). The predicted amino acid sequence disclosed herein for AQ73_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted AQ73_3 protein demonstrated at least some similarity to sequences identified as D16431 (hepatoma-derived GF [Homo sapiens]), D63707 (mouse hepatoma derived growth factor (HDGF) [Mus musculus]), R66727 (Human hepatoma derived growth factor), U18997 (ORF_f299 [Escherichia coli]), U97193 (similar to S. cerevisiae SIR2 (SP P06700) and mouse hepatoma derived growth factor HDGF (NID g945418) [Caenorhabditis elegans]), and W09404 (Human hepatoma-derived growth factor (HDGF-2)). Based upon sequence similarity, AQ73_3 proteins and each similar protein or peptide may share at least some activity.

AQ73_3 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 67 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "BG142_1"

A polynucleotide of the present invention has been identified as clone "BG142_1". BG142_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BG142_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BG142_1 protein").

The nucleotide sequence of BG142_1 as presently determined is reported in SEQ ID NO:138, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BG142_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:139.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BG142_1 should be approximately 1100 bp.

The nucleotide sequence disclosed herein for BG142_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BG142_1 demonstrated at least some similarity with sequences identified as AA170261 (ms87h11.r1 Soares mouse 3NbMS Mus musculus cDNA clone 618597 5' similar to TR E245601 E245601 G-RICH BOX-BINDING PROTEIN), L04282 (Human CACCC box-binding protein mRNA, complete cds), N27696 (yx51h12.r1 Homo sapiens cDNA clone 265319 5'), W96110 (ze09a11.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 358460 5'), and W96111 (ze09a11.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 358460 3'). The predicted amino acid sequence disclosed herein for BG142_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BG142_1 protein demonstrated at least some similarity to sequences identified as U80078 (transcription factor BFCOL1 [Mus musculus]) and X98096 (G-rich box-binding protein [Mus musculus]). Based upon sequence similarity, BG142_1 proteins and each similar protein or peptide may share at least some activity.

Clone "BV66_1"

A polynucleotide of the present invention has been identified as clone "BV66_1". BV66_1 was isolated from a human adult brain cDNA library using methods which are selective

for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BV66_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BV66_1 protein").

The nucleotide sequence of BV66_1 as presently determined is reported in SEQ ID NO:140, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BV66_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:141.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BV66_1 should be approximately 870 bp.

The nucleotide sequence disclosed herein for BV66_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database. The nucleotide sequence of BV66_1 indicates that it may contain a TAAA1 simple repeat element.

Clone "BV291_3"

A polynucleotide of the present invention has been identified as clone "BV291_3". BV291_3 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BV291_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BV291_3 protein").

The nucleotide sequence of BV291_3 as presently determined is reported in SEQ ID NO:142, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BV291_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:143.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BV291_3 should be approximately 2000 bp.

The nucleotide sequence disclosed herein for BV291_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BV291_3 demonstrated at least some similarity with sequences identified as H10954 (ym06e09.r1 Homo sapiens cDNA clone 47034 5'), H10955 (ym06e09.s1 Homo sapiens cDNA clone 47034 3'), N25300 (yw52c10.s1 Homo sapiens cDNA clone 255858 3'), T25940 (Human gene signature HUMGS08173), T68890 (yc30g11.s1 Homo sapiens cDNA clone 82244 3'), T78286 (yc99a08.r1 Homo sapiens cDNA clone 24033 5'), Z39987 (H. sapiens partial cDNA

sequence; clone c-1oh05), and Z47073 (Caenorhabditis elegans cosmid ZC506). The predicted amino acid sequence disclosed herein for BV291_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BV291_3 protein demonstrated at least some similarity to sequences identified as X02155 (BTTGR_1 thyroglobulin [Bos taurus]). Based upon sequence similarity, BV291_3 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the BV291_3 protein sequence centered around amino acid 48 of SEQ ID NO:143.

BV291_3 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 30 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

Clone "CK201_1"

A polynucleotide of the present invention has been identified as clone "CK201_1". CK201_1 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CK201_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CK201_1 protein").

The nucleotide sequence of CK201_1 as presently determined is reported in SEQ ID NO:144, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CK201_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:145.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CK201_1 should be approximately 1080 bp.

The nucleotide sequence disclosed herein for CK201_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CK201_1 demonstrated at least some similarity with sequences identified as AA129133 (zo09h12.s1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone 567239 3' similar to contains Alu repetitive element), D81444 (Human fetal brain cDNA 5'-end GEN-164G10), R36326 (yg69h09.r1 Homo sapiens cDNA clone 38821 5'), T08553 (Oncogene R-ras mutant cDNA (exons 2-6)), T31595 (Probe (BLUR13) for Alu repeat sequence), X03273 (Human Alu-family cluster 5' of alpha(1)-acid glycoprotein gene), and X69907 (H.sapiens gene for mitochondrial ATP synthase c subunit). The predicted amino acid sequence disclosed herein for CK201_1 was searched against the GenPept and GeneSeq amino acid

sequence databases using the BLASTX search protocol. The predicted CK201_1 protein demonstrated at least some similarity to sequences identified as D21827 (major surface glycoprotein [Pneumocystis carinii]). Based upon sequence similarity, CK201_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of CK201_1 indicates that it may contain an Alu repetitive element.

CK201_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 40 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "CQ331_2"

A polynucleotide of the present invention has been identified as clone "CQ331_2". CQ331_2 was isolated from a human adult heart cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CQ331_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CQ331_2 protein").

The nucleotide sequence of CQ331_2 as presently determined is reported in SEQ ID NO:146, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CQ331_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:147. Amino acids 7 to 19 of SEQ ID NO:147 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 20. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CQ331_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CQ331_2 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for CQ331_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CQ331_2 demonstrated at least some similarity with sequences identified as J03766 (Canine cardiac calsequestrin mRNA, complete cds), L29766 (Homo sapiens epoxide hydrolase (EPHX) gene, complete cds), N83601 (KK1173F Homo sapiens cDNA clone KK1173 5' similar to CALSEQUESTRIN (CARDIAC)), T99646 (ye73f12.s1 Homo sapiens cDNA clone 123407 3' similar to contains Alu repetitive element;contains PTR5 repetitive element), and W76326 (zd60d04.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 345031 5' similar to contains Alu repetitive element). The predicted amino acid sequence disclosed herein for

CQ331_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CQ331_2 protein demonstrated at least some similarity to sequences identified as J03766 (DOGCAL_1 Canine cardiac calsequestrin mRNA, complete cds [Canis canis]) and X55040 (calsequestrin [Oryctolagus cuniculus]). Based upon sequence similarity, CQ331_2 proteins and each similar protein or peptide may share at least some activity.

Clone "CT550_1"

A polynucleotide of the present invention has been identified as clone "CT550_1". CT550_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CT550_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CT550_1 protein").

The nucleotide sequence of CT550_1 as presently determined is reported in SEQ ID NO:148, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CT550_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:149.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CT550_1 should be approximately 1070 bp.

The nucleotide sequence disclosed herein for CT550_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database. The TopPredII computer program predicts a potential transmembrane domain within the CT550_1 protein sequence centered around amino acid 25 of SEQ ID NO:149.

CT550_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 7 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "CT585_1"

A polynucleotide of the present invention has been identified as clone "CT585_1". CT585_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence

of the encoded protein. CT585_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CT585_1 protein").

The nucleotide sequence of CT585_1 as presently determined is reported in SEQ ID NO:150, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CT585_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:151. Amino acids 2 to 14 of SEQ ID NO:151 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 15. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CT585_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CT585_1 should be approximately 2710 bp.

The nucleotide sequence disclosed herein for CT585_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CT585_1 demonstrated at least some similarity with sequences identified as AA069442 (zf74b02.s1 Soares pineal gland N3HPG Homo sapiens cDNA clone 382635 3'), L38961 (Homo sapiens putative transmembrane protein (B5) mRNA, complete cds), N34932 (yy49b10.s1 Homo sapiens cDNA clone 276859 3'), N60101 (TgESTzy11f10.r1 Toxoplasma gondii cDNA clone tgzy11f10.r1 5'), and U13019 (Caenorhabditis elegans cosmid T12A2). The predicted amino acid sequence disclosed herein for CT585_1 was searched against the GenPept, GeneSeq, and SwissProt amino acid sequence databases using the BLASTX search protocol. The predicted CT585_1 protein demonstrated at least some similarity to sequences identified as L34260 (transmembrane protein [Mus musculus]), L38961 (transmembrane protein [Homo sapiens]), P46975 (Caenorhabditis elegans oligosaccharyl transferase stt3 [Caenorhabditis elegans]), and U13019 (Caenorhabditis elegans cosmid T12A2 [Caenorhabditis elegans]). Based upon sequence similarity, CT585_1 proteins and each similar protein or peptide may share at least some activity.

Clone "CT797_3"

A polynucleotide of the present invention has been identified as clone "CT797_3". CT797_3 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CT797_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CT797_3 protein").

The nucleotide sequence of CT797_3 as presently determined is reported in SEQ ID NO:152, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CT797_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:153.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CT797_3 should be approximately 3300 bp.

The nucleotide sequence disclosed herein for CT797_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CT797_3 demonstrated at least some similarity with sequences identified as AA573847 (nk08d06.s1 NCI_CGAP_Co2 Homo sapiens cDNA clone IMAGE:1012907). The predicted amino acid sequence disclosed herein for CT797_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CT797_3 protein demonstrated at least some similarity to sequences identified as U18309 (chromokinesin [Gallus gallus]) and Z82271 (T01G1.1 [Caenorhabditis elegans]). Based upon sequence similarity, CT797_3 proteins and each similar protein or peptide may share at least some activity.

CT797_3 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 80 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

Clone "CB107_1"

A polynucleotide of the present invention has been identified as clone "CB107_1". CB107_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CB107_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CB107_1 protein").

The nucleotide sequence of the 5' portion of CB107_1 as presently determined is reported in SEQ ID NO:154. An additional internal nucleotide sequence from CB107_1 as presently determined is reported in SEQ ID NO:155. What applicants believe is the proper reading frame and the predicted amino acid sequence encoded by such internal sequence is reported in SEQ ID NO:156. Additional nucleotide sequence from the 3' portion of CB107_1, including a poly(A) tail, is reported in SEQ ID NO:157.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CB107_1 should be approximately 3300 bp.

The nucleotide sequence disclosed herein for CB107_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CB107_1 demonstrated at least some similarity with sequences identified as AA121485 (zn80a02.s1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone 564458 3'), AA428192 (zw51b08.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 773559 3'), D83018 (Human mRNA for nel-related protein 2, complete cds), F10919 (H. sapiens partial cDNA sequence; clone c-31g01), H15375 (ym28d09.r1 Homo sapiens cDNA clone 49527 5' similar to SP A54105 A54105 FIBRILLIN-2 PRECURSOR), U48245 (Rattus norvegicus protein kinase C-binding protein Nel mRNA, complete cds), U59230 (Mus musculus mel (MEL91) mRNA, complete cds), and W28387 (46c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA). The predicted amino acid sequence disclosed herein for CB107_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CB107_1 protein demonstrated at least some similarity to sequences identified as D83018 (nel-related protein 2 [Homo sapiens]), R05222 (Antigen GX5401FL encoded by Eimeria tenella genomic DNA), R79964 (Connective tissue growth factor), U48245 (RNU48245_1 protein kinase C-binding protein Nel [Rattus norvegicus]), and U59230 (mel [Mus musculus]). Based upon sequence similarity, CB107_1 proteins and each similar protein or peptide may share at least some activity.

Clone "CG300_3"

A polynucleotide of the present invention has been identified as clone "CG300_3". CG300_3 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CG300_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CG300_3 protein").

The nucleotide sequence of CG300_3 as presently determined is reported in SEQ ID NO:158, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CG300_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:159. Amino acids 30 to 42 of SEQ ID NO:159 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 43. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CG300_3 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CG300_3 should be approximately 1800 bp.

The nucleotide sequence disclosed herein for CG300_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CG300_3 demonstrated at least some similarity with sequences identified as N40185 (yy44d08.s1 Homo sapiens cDNA clone 276399 3') and W01791 (za72d06.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 298091 5'). Based upon sequence similarity, CG300_3 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts four potential transmembrane domains within the CG300_3 protein sequence, centered around amino acids 34, 98, 151, and 179 of SEQ ID NO:159, respectively.

CG300_3 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 29 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "CJ145_1"

A polynucleotide of the present invention has been identified as clone "CJ145_1". CJ145_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CJ145_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CJ145_1 protein").

The nucleotide sequence of CJ145_1 as presently determined is reported in SEQ ID NO:160, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CJ145_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:161. Amino acids 6 to 18 of SEQ ID NO:161 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 19. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CJ145_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CJ145_1 should be approximately 3600 bp.

The nucleotide sequence disclosed herein for CJ145_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search

protocols. CJ145_1 demonstrated at least some similarity with sequences identified as R43655 (yc86b04.s1 Homo sapiens cDNA clone 22829 3'), R50995 (yg63f06.s1 Homo sapiens cDNA clone 37377 3' similar to contains MER22 repetitive element), and W92748 (zd92h03.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 356981 3'). Based upon sequence similarity, CJ145_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of CJ145_1 indicates that it may contain a CA simple repeat element.

Clone "CJ160_11"

A polynucleotide of the present invention has been identified as clone "CJ160_11". CJ160_11 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CJ160_11 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CJ160_11 protein").

The nucleotide sequence of CJ160_11 as presently determined is reported in SEQ ID NO:162, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CJ160_11 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:163. Amino acids 17 to 29 of SEQ ID NO:163 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 30. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CJ160_11 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CJ160_11 should be approximately 1700 bp.

The nucleotide sequence disclosed herein for CJ160_11 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CJ160_11 demonstrated at least some similarity with sequences identified as AA024511 (ze76e04.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 364926 3') and AC000074 (00884; HTGS phase 3, complete sequence). Based upon sequence similarity, CJ160_11 proteins and each similar protein or peptide may share at least some activity.

CJ160_11 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 96 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

Clone "CO20_1"

A polynucleotide of the present invention has been identified as clone "CO20_1". CO20_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CO20_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CO20_1 protein").

The nucleotide sequence of the 5' portion of CO20_1 as presently determined is reported in SEQ ID NO:164. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:165. The predicted amino acid sequence of the CO20_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:165. Amino acids 17 to 29 of SEQ ID NO:165 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 30. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CO20_1 protein. Additional nucleotide sequence from the 3' portion of CO20_1, including a poly(A) tail, is reported in SEQ ID NO:166.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CO20_1 should be approximately 2400 bp.

The nucleotide sequence disclosed herein for CO20_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CO20_1 demonstrated at least some similarity with sequences identified as AA045770 (zl68b10.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 509755 3' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A), AA070899 (zm66c01.s1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone 530592 3' similar to contains Alu repetitive element), AA325205 (EST28155 Cerebellum II Homo sapiens cDNA 5' end), N22253 (yw36a08.s1 Homo sapiens cDNA clone 254294 3' similar to SP S29539 S29539 BASIC PROTEIN, 23K), R01933 (ye85g07.s1 Homo sapiens cDNA clone 124572 3' similar to SP:S29539 S29539 BASIC PROTEIN, 23K), R12008 (yf51f04.r1 Homo sapiens cDNA clone 25456 5'), R39848 (yf51f04.s1 Homo sapiens cDNA clone 25456 3' similar to contains Alu repetitive element;contains PTR5 repetitive element), R56565 (yg91c12.r1 Homo sapiens cDNA clone 40891 5'), T19487 (Human gene signature HUMGS00543), T30988 (EST25695 Homo sapiens cDNA 5' end similar to None), U37026 (Rattus norvegicus brain sodium channel beta 2 subunit (SCNB2) mRNA, complete cds), and X56932 (H.sapiens mRNA for 23 kD highly basic protein). The predicted amino acid sequence disclosed herein for CO20_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol.

The predicted CO20_1 protein demonstrated at least some similarity to sequences identified as U37026 (sodium channel beta 2 subunit [Rattus norvegicus]), U58658 (unknown [Homo sapiens]), and X56932 (23 kD highly basic protein [Homo sapiens]). The sodium channel beta 2 subunit is a glycoprotein with an extracellular domain containing an immunoglobulin-like fold with similarity to the neural cell adhesion molecule contactin. Based upon sequence similarity, CO20_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of CO20_1 indicates that it may contain an Alu repetitive element.

Clone "CO223_3"

A polynucleotide of the present invention has been identified as clone "CO223_3". CO223_3 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CO223_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CO223_3 protein").

The nucleotide sequence of CO223_3 as presently determined is reported in SEQ ID NO:167, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CO223_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:168. Amino acids 35 to 47 of SEQ ID NO:168 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 48. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CO223_3 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CO223_3 should be approximately 700 bp.

The nucleotide sequence disclosed herein for CO223_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CO223_3 demonstrated at least some similarity with sequences identified as AA004498 (zh87b06.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 428243 5' similar to gb M62505 C5A ANAPHYLATOXIN CHEMOTACTIC RECEPTOR (HUMAN);contains L1.t1 L1 repetitive element) and U47924 (Human chromosome 12p13 gene cluster, surface antigen CD4 (CD4), A, B, G-protein beta-3 subunit (GNB3), isopeptidase T (ISOT) and triosephosphate isomerase (TPI) genes, complete cds). Based upon sequence similarity, CO223_3 proteins and each similar protein or peptide may share at least some activity.

The 3' end of the CO223_3 polynucleotide sequence contains a 54-bp sequence that is repeated three times in the clone; these repeats begin at positions 314, 368, and 422 of SEQ ID NO:167 and encode amino acids 47 to 64, 65 to 82, and 83 to 99 of SEQ ID NO:168, respectively.

Clone "CO310_2"

A polynucleotide of the present invention has been identified as clone "CO310_2". CO310_2 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CO310_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CO310_2 protein").

The nucleotide sequence of CO310_2 as presently determined is reported in SEQ ID NO:169, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CO310_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:170.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CO310_2 should be approximately 1400 bp.

The nucleotide sequence disclosed herein for CO310_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database. The nucleotide sequence of CO310_2 indicates that it may contain an L1 repetitive element.

Clone "CP258_3"

A polynucleotide of the present invention has been identified as clone "CP258_3". CP258_3 was isolated from a human adult salivary gland cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CP258_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CP258_3 protein").

The nucleotide sequence of CP258_3 as presently determined is reported in SEQ ID NO:171, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CP258_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:172. Amino acids 3 to 15 of SEQ ID NO:172 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 16. Due to the hydrophobic nature of the predicted leader/signal

sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CP258_3 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CP258_3 should be approximately 560 bp.

The nucleotide sequence disclosed herein for CP258_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database.

CP258_3 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 26 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "CW1155_3"

A polynucleotide of the present invention has been identified as clone "CW1155_3". CW1155_3 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CW1155_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CW1155_3 protein").

The nucleotide sequence of CW1155_3 as presently determined is reported in SEQ ID NO:173, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CW1155_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:174. Amino acids 220 to 232 of SEQ ID NO:174 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 233. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CW1155_3 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CW1155_3 should be approximately 1170 bp.

The nucleotide sequence disclosed herein for CW1155_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CW1155_3 demonstrated at least some similarity with sequences identified as AA169043 (ms36h08.r1 Stratagene mouse heart (#937316) Mus musculus cDNA clone 613695 5'), D86145 (Rat mRNA), and H29261 (ym32b03.s1 Homo sapiens cDNA clone 49733 3'). Based upon sequence similarity, CW1155_3 proteins and each similar protein or peptide may share at least some activity.

Clone "CZ247_2"

A polynucleotide of the present invention has been identified as clone "CZ247_2". CZ247_2 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CZ247_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CZ247_2 protein").

The nucleotide sequence of CZ247_2 as presently determined is reported in SEQ ID NO:175, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CZ247_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:176. Amino acids 545 to 557 of SEQ ID NO:176 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 558. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CZ247_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CZ247_2 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for CZ247_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CZ247_2 demonstrated at least some similarity with sequences identified as T09256 (Human ara Kb beta-galactosidase fusion protein coding sequence), W27222 (26h9 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA), and W72736 (zd71e02.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 346106 3'). The predicted amino acid sequence disclosed herein for CZ247_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CZ247_2 protein demonstrated at least some similarity to sequences identified as R88069 (Human ara Kb beta-galactosidase fusion protein). Based upon sequence similarity, CZ247_2 proteins and each similar protein or peptide may share at least some activity.

Clone "AM666_1"

A polynucleotide of the present invention has been identified as clone "AM666_1". AM666_1 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino

acid sequence of the encoded protein. AM666_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AM666_1 protein").

The nucleotide sequence of AM666_1 as presently determined is reported in SEQ ID NO:177, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the AM666_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:178. Amino acids 15 to 27 of SEQ ID NO:178 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 28. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the AM666_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AM666_1 should be approximately 1300 bp.

The nucleotide sequence disclosed herein for AM666_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. AM666_1 demonstrated at least some similarity with sequences identified as AA493985 (nh07g08.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone). Based upon sequence similarity, AM666_1 proteins and each similar protein or peptide may share at least some activity.

AM666_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 17 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "BN387_3"

A polynucleotide of the present invention has been identified as clone "BN387_3". BN387_3 was isolated from a human adult placenta cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BN387_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BN387_3 protein").

The nucleotide sequence of BN387_3 as presently determined is reported in SEQ ID NO:179, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BN387_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:180. Amino acids 14 to 26 of SEQ ID NO:180 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 27. Due to the hydrophobic nature of the predicted leader/signal

sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the BN387_3 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BN387_3 should be approximately 2000 bp.

The nucleotide sequence disclosed herein for BN387_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BN387_3 demonstrated at least some similarity with sequences identified as H16912 (ym39d01.r1 Homo sapiens cDNA clone 50771 5'). Based upon sequence similarity, BN387_3 proteins and each similar protein or peptide may share at least some activity.

BN387_3 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 30 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

Clone "BQ135_2"

A polynucleotide of the present invention has been identified as clone "BQ135_2". BQ135_2 was isolated from a human adult colon (adenocarcinoma Caco2) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BQ135_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BQ135_2 protein").

The nucleotide sequence of BQ135_2 as presently determined is reported in SEQ ID NO:181, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BQ135_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:182.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BQ135_2 should be approximately 1200 bp.

The nucleotide sequence disclosed herein for BQ135_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BQ135_2 demonstrated at least some similarity with sequences identified as AA023751 (mh81f01.r1 Soares mouse placenta 4NbMP13.5 14.5 Mus musculus cDNA clone 457369 5'), AA105433 (ml83g01.r1 Stratagene mouse kidney (#937315) Mus musculus cDNA clone 518640 5'), D64061 (Rat brain mRNA for annexin V-binding protein (ABP-7), partial cds), and N67257 (yz49b08.s1 Homo sapiens cDNA clone 286359 3'). The predicted amino acid sequence disclosed herein for BQ135_2 was searched against the GenPept and GeneSeq amino

acid sequence databases using the BLASTX search protocol. The predicted BQ135_2 protein demonstrated at least some similarity to sequences identified as D64061 (annexin V-binding protein (ABP-7) [Rattus norvegicus]). Annexins associate with membranes and act as ion channels, they can also act as an autocrine factor that enhances osteoclast formation and bone resorption. Annexins have been localized in nucleoli and mitochondria but also in the cytoplasm, plasma (i.e. blood) and in association with vesicles. They are probably involved in fusing vesicles to each other and to plasma membranes causing secretion of vesicular contents. Specifically they have a calcium-dependent ability to bind phospholipids. Thus they are membrane associated. It is possible that annexin-binding proteins are also membrane associated even though they are highly hydrophilic through the same mechanism (electrostatic interaction with phospholipids of membranes). Based upon sequence similarity, BQ135_2 proteins and each similar protein or peptide may share at least some activity.

Clone "CR678_1"

A polynucleotide of the present invention has been identified as clone "CR678_1". CR678_1 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CR678_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CR678_1 protein").

The nucleotide sequence of CR678_1 as presently determined is reported in SEQ ID NO:183, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CR678_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:184.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CR678_1 should be approximately 870 bp.

The nucleotide sequence disclosed herein for CR678_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CR678_1 demonstrated at least some similarity with sequences identified as X85232 (H.sapiens chromosome 3 sequences). Based upon sequence similarity, CR678_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of CR678_1 indicates that it may contain an Alu repetitive element.

Clone "CW420_2"

A polynucleotide of the present invention has been identified as clone "CW420_2". CW420_2 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CW420_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CW420_2 protein").

The nucleotide sequence of CW420_2 as presently determined is reported in SEQ ID NO:185, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CW420_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:186.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CW420_2 should be approximately 5100 bp.

The nucleotide sequence disclosed herein for CW420_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CW420_2 demonstrated at least some similarity with sequences identified as T55440 (yb38e09.s1 Homo sapiens cDNA clone 73480 3'). Based upon sequence similarity, CW420_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the CW420_2 protein sequence centered around amino acids 500 and 1270 of SEQ ID NO:186, respetively.

Clone "CW795_2"

A polynucleotide of the present invention has been identified as clone "CW795_2". CW795_2 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CW795_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CW795_2 protein").

The nucleotide sequence of CW795_2 as presently determined is reported in SEQ ID NO:187, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CW795_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:188.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CW795_2 should be approximately 3000 bp.

The nucleotide sequence disclosed herein for CW795_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA

search protocols. CW795_2 demonstrated at least some similarity with sequences identified as AA115676 (zl86a09.s1 Stratagene colon (#937204) Homo sapiens cDNA clone 511480 3'), N22955 (yw44h07.s1 Homo sapiens cDNA clone 255133 3'), and W56804 (zd16g06.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 340858 3'). The predicted amino acid sequence disclosed herein for CW795_2 was searched against the GenPept, GeneSeq, and SwissProt amino acid sequence databases using the BLASTX search protocol. The predicted CW795_2 protein demonstrated at least some similarity to sequences identified as X81068 (probable mitochondrial protein) and the yeast proteins rca1 and afg3 (tat-binding homologues). Based upon sequence similarity, CW795_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the CW795_2 protein sequence centered around amino acids 60 and 170 of SEQ ID NO:188, respectively.

CW795_2 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 10 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "CW823_3"

A polynucleotide of the present invention has been identified as clone "CW823_3". CW823_3 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CW823_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CW823_3 protein").

The nucleotide sequence of CW823_3 as presently determined is reported in SEQ ID NO:189, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CW823_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:190.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CW823_3 should be approximately 600 bp.

The nucleotide sequence disclosed herein for CW823_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database.

Clone "DF989_3"

A polynucleotide of the present invention has been identified as clone "DF989_3". DF989_3 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. DF989_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "DF989_3 protein").

The nucleotide sequence of the 5' portion of DF989_3 as presently determined is reported in SEQ ID NO:191. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:192. The predicted amino acid sequence of the DF989_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:192. Amino acids 2 to 14 of SEQ ID NO:192 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 15. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the DF989_3 protein. Additional nucleotide sequence from the 3' portion of DF989_3, including a poly(A) tail, is reported in SEQ ID NO:193.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone DF989_3 should be approximately 1800 bp.

The nucleotide sequence disclosed herein for DF989_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. DF989_3 demonstrated at least some similarity with sequences identified as R24724 (yg43c05.r1 Homo sapiens cDNA clone 35337 5') and T33717 (EST58870 Homo sapiens cDNA 5' end similar to None). Based upon sequence similarity, DF989_3 proteins and each similar protein or peptide may share at least some activity.

Clone "DL162_1"

A polynucleotide of the present invention has been identified as clone "DL162_1". DL162_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. DL162_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "DL162_1 protein").

The nucleotide sequence of DL162_1 as presently determined is reported in SEQ ID NO:194, and includes a poly(A) tail. What applicants presently believe to be the proper reading

frame and the predicted amino acid sequence of the DL162_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:195. Amino acids 28 to 40 of SEQ ID NO:195 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 41. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the DL162_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone DL162_1 should be approximately 875 bp.

The nucleotide sequence disclosed herein for DL162_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database.

Clone "DL162_2"

A polynucleotide of the present invention has been identified as clone "DL162_2". DL162_2 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. DL162_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "DL162_2 protein").

The nucleotide sequence of DL162_2 as presently determined is reported in SEQ ID NO:196, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the DL162_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:197. Amino acids 1 to 13 of SEQ ID NO:197 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 14. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the DL162_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone DL162_2 should be approximately 4000 bp.

The predicted amino acid sequence disclosed herein for DL162_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted DL162_2 protein demonstrated at least some similarity to sequences identified as AB002309 (KIAA0311 protein [Homo sapiens]). The TopPredII computer program predicts a potential transmembrane domains within the DL162_2 protein sequence near the carboxyl terminus of SEQ ID NO:197.

DL162_2 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 160 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "EC172_1"

A polynucleotide of the present invention has been identified as clone "EC172_1". EC172_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. EC172_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "EC172_1 protein").

The nucleotide sequence of EC172_1 as presently determined is reported in SEQ ID NO:198, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the EC172_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:199. Amino acids 659 to 671 of SEQ ID NO:199 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 672. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the EC172_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone EC172_1 should be approximately 4000 bp.

The nucleotide sequence disclosed herein for EC172_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. EC172_1 demonstrated at least some similarity with sequences identified as H31192 (EST104991 Rattus sp. cDNA 3' end similar to C.elegans hypothetical protein ZK1098.10) and U29585 (Streptococcus pyogenes emm18.1). The predicted amino acid sequence disclosed herein for EC172_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted EC172_1 protein demonstrated at least some similarity to sequences identified as Z22176 (ZK1098.10 [Caenorhabditis elegans]). Based upon sequence similarity, EC172_1 proteins and each similar protein or peptide may share at least some activity.

Deposit of Clones

Clones AX65_22, BD335_14, BG241_1, BL187_4, BL249_18, BO71_1, BO365_2, BV51_1, BV140_3, BV141_2, CC194_4, and DA136_11 were deposited on October 3, 1996 with

the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98196, from which each clone comprising a particular polynucleotide is obtainable.

Clones AR415_4, AS63_29, BG160_1, BO432_4, BO538_2, BR595_4, CI490_2, CI522_1, CN238_1, CO390_1, and AY304_1 (an additional isolate of clone AY304_14) were deposited on October 25, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98232, from which each clone comprising a particular polynucleotide is obtainable. Clone AY304_14 wasdeposited on October 23, 1997 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and was given the accession number 98561.

Clones AJ20_2, AR440_1, AS164_1, AX8_1, BD176_3, BD339_1, BD427_1, BL229_22, BV123_16, and CH377_1 were deposited on November 15, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98261, from which each clone comprising a particular polynucleotide is obtainable.

Clones BD441_1, BD441_2, BG102_3, BK158_1, BP163_1, BZ16_3, CC182_1, CG109_1 and CJ397_1 were deposited on November 20, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98264, from which each clone comprising a particular polynucleotide is obtainable.

Clones AM795_4, AT340_1, BG132_1, BG219_2, BG366_2, BV172_2, CC247_10, CI480_9, CO722_1, and CT748_2 were deposited on December 5, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98271, from which each clone comprising a particular polynucleotide is obtainable.

Clones AJ1_1, AQ73_3, BG142_1, BV66_1, BV291_3, CK201_1, CQ331_2, CT550_1, CT585_1 and CT797_3 were deposited on December 13, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98278, from which each clone comprising a particular polynucleotide is obtainable.

Clones CB107_1, CG300_3, CJ145_1, CJ160_11, CO20_1, CO223_1, CO310_2, CP258_3, CW1155_3 and CZ247_2 were deposited on December 17, 1996 with the ATCC

(American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98279, from which each clone comprising a particular polynucleotide is obtainable. Clone CO223_3 was deposited on January 9, 1997 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and was given the accession number 98291.

Clones AM666_1, BN387_3, BQ135_2, CR678_1, CW420_2, CW795_2, CW823_3, DF989_3, DL162_2, DL162_1, and EC172_1 were deposited on January 10, 1997 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98292, from which each clone comprising a particular polynucleotide is obtainable.

All restrictions on the availability to the public of the deposited material will be irrevocably removed upon the granting of the patent, except for the requirements specified in 37 C.F.R. § 1.808(b), and the term of the deposit will comply with 37 C.F.R. § 1.806.

Each clone has been transfected into separate bacterial cells (*E. coli*) in this composite deposit. Each clone can be removed from the vector in which it was deposited by performing an EcoRI/NotI digestion (5' site, EcoRI; 3' site, NotI) to produce the appropriate fragment for such clone. Each clone was deposited in either the pED6 or pNOTs vector depicted in Figures 1A and 1B, respectively. The pED6dpc2 vector ("pED6") was derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning (Kaufman *et al.*, 1991, *Nucleic Acids Res.* 19: 4485-4490); the pNOTs vector was derived from pMT2 (Kaufman *et al.*, 1989, *Mol. Cell. Biol.* 9: 946-958) by deletion of the DHFR sequences, insertion of a new polylinker, and insertion of the M13 origin of replication in the ClaI site. In some instances, the deposited clone can become "flipped" (i.e., in the reverse orientation) in the deposited isolate. In such instances, the cDNA insert can still be isolated by digestion with EcoRI and NotI. However, NotI will then produce the 5' site and EcoRI will produce the 3' site for placement of the cDNA in proper orientation for expression in a suitable vector. The cDNA may also be expressed from the vectors in which they were deposited.

Bacterial cells containing a particular clone can be obtained from the composite deposit as follows:

An oligonucleotide probe or probes should be designed to the sequence that is known for that particular clone. This sequence can be derived from the sequences provided herein, or from a combination of those sequences. The sequence of an oligonucleotide probe that was used to isolate or to sequence each full-length clone is identified below, and should be most reliable in isolating the clone of interest.

Clone	Probe Sequence
AX65_22	SEQ ID NO:200
BD335_14	SEQ ID NO:201
BG241_1	SEQ ID NO:202
BL187_4	SEQ ID NO:203
BL249_18	SEQ ID NO:204
BO71_1	SEQ ID NO:205
BO365_2	SEQ ID NO:206
BV51_1	SEQ ID NO:207
BV140_3	SEQ ID NO:208
BV141_2	SEQ ID NO:209
CC194_4	SEQ ID NO:210
DA136_11	SEQ ID NO:211
AR415_4	SEQ ID NO:212
AS63_29	SEQ ID NO:213
AY304_14	SEQ ID NO:214
BG160_1	SEQ ID NO:215
BO432_4	SEQ ID NO:216
BO538_2	SEQ ID NO:217
BR595_4	SEQ ID NO:218
CI490_2	SEQ ID NO:219
CI522_1	SEQ ID NO:220
CN238_1	SEQ ID NO:221
CO390_1	SEQ ID NO:222
AJ20_2	SEQ ID NO:223
AR440_1	SEQ ID NO:224
AS164_1	SEQ ID NO:225
AX8_1	SEQ ID NO:226
BD176_3	SEQ ID NO:227
BD339_1	SEQ ID NO:228
BD427_1	SEQ ID NO:229
BL229_22	SEQ ID NO:230
BV123_16	SEQ ID NO:231
CH377_1	SEQ ID NO:232
BD441_1	SEQ ID NO:233

BD441_2	SEQ ID NO:234
BG102_3	SEQ ID NO:235
BK158_1	SEQ ID NO:236
BP163_1	SEQ ID NO:237
BZ16_3	SEQ ID NO:238
CC182_1	SEQ ID NO:239
CG109_1	SEQ ID NO:240
CJ397_1	SEQ ID NO:241
AM795_4	SEQ ID NO:242
AT340_1	SEQ ID NO:243
BG132_1	SEQ ID NO:244
BG219_2	SEQ ID NO:245
BG366_2	SEQ ID NO:246
BV172_2	SEQ ID NO:247
CC247_10	SEQ ID NO:248
CI480_9	SEQ ID NO:249
CO722_1	SEQ ID NO:250
CT748_2	SEQ ID NO:251
AJ1_1	SEQ ID NO:252
AQ73_3	SEQ ID NO:253
BG142_1	SEQ ID NO:254
BV66_1	SEQ ID NO:255
BV291_3	SEQ ID NO:256
CK201_1	SEQ ID NO:257
CQ331_2	SEQ ID NO:258
CT550_1	SEQ ID NO:259
CT585_1	SEQ ID NO:260, SEQ ID NO:262
CT797_3	SEQ ID NO:261
CB107_1	SEQ ID NO:263
CG300_3	SEQ ID NO:264
CJ145_1	SEQ ID NO:265
CJ160_11	SEQ ID NO:266
CO20_1	SEQ ID NO:267
CO223_3	SEQ ID NO:268
CO310_2	SEQ ID NO:269

CP258_3	SEQ ID NO:270
CW1155_3	SEQ ID NO:271
CZ247_2	SEQ ID NO:272
AM666_1	SEQ ID NO:273
BN387_3	SEQ ID NO:274
BQ135_2	SEQ ID NO:275
CR678_1	SEQ ID NO:276
CW420_2	SEQ ID NO:277
CW795_2	SEQ ID NO:278
CW823_3	SEQ ID NO:279
DF989_3	SEQ ID NO:280
DL162_1, DL162_2	SEQ ID NO:281
EC172_1	SEQ ID NO:282

In the sequences listed above which include an N at position 2, that position is occupied in preferred probes/primers by a biotinylated phosphoaramidite residue rather than a nucleotide (such as, for example, that produced by use of biotin phosphoramidite (1-dimethoxytrityloxy-2-(N-biotinyl-4-aminobutyl)-propyl-3-O-(2-cyanoethyl)-(N,N-diisopropyl)-phosphoramadite) (Glen Research, cat. no. 10-1953)).

The design of the oligonucleotide probe should preferably follow these parameters:

(a) It should be designed to an area of the sequence which has the fewest ambiguous bases ("N's"), if any;

(b) It should be designed to have a T_m of approx. 80 ° C (assuming 2° for each A or T and 4 degrees for each G or C).

The oligonucleotide should preferably be labeled with γ-^{32}P ATP (specific activity 6000 Ci/mmole) and T4 polynucleotide kinase using commonly employed techniques for labeling oligonucleotides. Other labeling techniques can also be used. Unincorporated label should preferably be removed by gel filtration chromatography or other established methods. The amount of radioactivity incorporated into the probe should be quantitated by measurement in a scintillation counter. Preferably, specific activity of the resulting probe should be approximately 4e+6 dpm/pmole.

The bacterial culture containing the pool of full-length clones should preferably be thawed and 100 µl of the stock used to inoculate a sterile culture flask containing 25 ml of sterile L-broth containing ampicillin at 100 µg/ml. The culture should preferably be grown to saturation at 37°C, and the saturated culture should preferably be diluted in fresh L-broth. Aliquots of these dilutions

should preferably be plated to determine the dilution and volume which will yield approximately 5000 distinct and well-separated colonies on solid bacteriological media containing L-broth containing ampicillin at 100 μg/ml and agar at 1.5% in a 150 mm petri dish when grown overnight at 37°C. Other known methods of obtaining distinct, well-separated colonies can also be employed.

Standard colony hybridization procedures should then be used to transfer the colonies to nitrocellulose filters and lyse, denature and bake them.

The filter is then preferably incubated at 65°C for 1 hour with gentle agitation in 6X SSC (20X stock is 175.3 g NaCl/liter, 88.2 g Na citrate/liter, adjusted to pH 7.0 with NaOH) containing 0.5% SDS, 100 μg/ml of yeast RNA, and 10 mM EDTA (approximately 10 mL per 150 mm filter). Preferably, the probe is then added to the hybridization mix at a concentration greater than or equal to 1e+6 dpm/mL. The filter is then preferably incubated at 65°C with gentle agitation overnight. The filter is then preferably washed in 500 mL of 2X SSC/0.5% SDS at room temperature without agitation, preferably followed by 500 mL of 2X SSC/0.1% SDS at room temperature with gentle shaking for 15 minutes. A third wash with 0.1X SSC/0.5% SDS at 65°C for 30 minutes to 1 hour is optional. The filter is then preferably dried and subjected to autoradiography for sufficient time to visualize the positives on the X-ray film. Other known hybridization methods can also be employed.

The positive colonies are picked, grown in culture, and plasmid DNA isolated using standard procedures. The clones can then be verified by restriction analysis, hybridization analysis, or DNA sequencing.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H.U. Saragovi, *et al.*, Bio/Technology 10, 773-778 (1992) and in R.S. McDowell, *et al.*, J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites. For example, fragments of the protein may be fused through "linker" sequences to the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein - IgM fusion would generate a decavalent form of the protein of the invention.

The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence listing by translation of the nucleotide sequence of each disclosed clone. The mature form(s) of such protein

may be obtained by expression of the disclosed full-length polynucleotide (preferably those deposited with the ATCC) in a suitable mammalian cell or other host cell. The sequence(s) of the mature form(s) of the protein may also be determinable from the amino acid sequence of the full-length form.

The present invention also provides genes corresponding to the polynucleotide sequences disclosed herein. "Corresponding genes" are the regions of the genome that are transcribed to produce the mRNAs from which cDNA polynucleotide sequences are derived and may include contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5' and 3' untranslated regions, alternatively spliced exons, introns, promoters, enhancers, and silencer or suppressor elements. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. An "isolated gene" is a gene that has been separated from the adjacent coding sequences, if any, present in the genome of the organism from which the gene was isolated.

The chromosomal location corresponding to the polynucleotide sequences disclosed herein may also be determined, for example by hybridizing appropriately labeled polynucleotides of the present invention to chromosomes *in situ*. It may also be possible to determine the corresponding chromosomal location for a disclosed polynucleotide by identifying significantly similar nucleotide sequences in public databases, such as expressed sequence tags (ESTs), that have already been mapped to particular chromosomal locations. For at least some of the polynucleotide sequences disclosed herein, public database sequences having at least some similarity to the polynucleotide of the present invention have been listed by database accession number. Searches using the GenBank accession numbers of these public database sequences can then be performed at an Internet site provided by the National Center for Biotechnology Information having the address http://www.ncbi.nlm.nih.gov/UniGene/, in order to identify "UniGene clusters" of overlapping sequences. Many of the "UniGene clusters" so identified will already have been mapped to particular chromosomal sites.

Organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein are provided. The desired change in gene expression can be achieved through the use of antisense polynucleotides or ribozymes that bind and/or cleave the mRNA transcribed from the gene (Albert and Morris, 1994, *Trends Pharmacol. Sci.* 15(7): 250-254; Lavarosky *et al.*, 1997, *Biochem. Mol. Med.* 62(1): 11-22; and Hampel, 1998, *Prog. Nucleic Acid Res. Mol. Biol.* **58**: 1-39; all of which are incorporated by

reference herein). The desired change in gene expression can also be achieved through the use of double-stranded ribonucleotide molecules having some complementarity to the mRNA transcribed from the gene, and which interfere with the transcription, stability, or expression of the mRNA ("RNA intereference" or "RNAi"; Fire *et al.*, 1998, *Nature* **391** (6669): 806-811; Montgomery *et al.*, 1998, *Proc. Natl. Acad. Sci. USA* **95** (26): 15502-15507; and Sharp, 1999, *Genes Dev.* **13** (2): 139-141; all of which are incorporated by reference herein). Transgenic animals that have multiple copies of the gene(s) corresponding to the polynucleotide sequences disclosed herein, preferably produced by transformation of cells with genetic constructs that are stably maintained within the transformed cells and their progeny, are provided. Transgenic animals that have modified genetic control regions that increase or reduce gene expression levels, or that change temporal or spatial patterns of gene expression, are also provided (see European Patent No. 0 649 464 B1, incorporated by reference herein). In addition, organisms are provided in which the gene(s) corresponding to the polynucleotide sequences disclosed herein have been partially or completely inactivated, through insertion of extraneous sequences into the corresponding gene(s) or through deletion of all or part of the corresponding gene(s). Partial or complete gene inactivation can be accomplished through insertion, preferably followed by imprecise excision, of transposable elements (Plasterk, 1992, *Bioessays* **14(9)**: 629-633; Zwaal *et al.*, 1993, *Proc. Natl. Acad. Sci. USA* **90(16)**: 7431-7435; Clark *et al.*, 1994, *Proc. Natl. Acad. Sci. USA* **91(2)**: 719-722; all of which are incorporated by reference herein), or through homologous recombination, preferably detected by positive/negative genetic selection strategies (Mansour *et al.*, 1988, *Nature* **336**: 348-352; U.S. Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153; 5,614, 396; 5,616,491; and 5,679,523; all of which are incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably are mammals. Such organisms are useful for the development of non-human models for the study of disorders involving the corresponding gene(s), and for the development of assay systems for the identification of molecules that interact with the protein product(s) of the corresponding gene(s).

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms, part or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information. For example, the TopPredII computer program can be used to predict the location of transmembrane domains in an amino acid sequence, domains

which are described by the location of the center of the transmsmbrane domain, with at least ten transmembrane amino acids on each side of the reported central residue(s).

Proteins and protein fragments of the present invention include proteins with amino acid sequence lengths that are at least 25%(more preferably at least 50%, and most preferably at least 75%) of the length of a disclosed protein and have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where sequence identity is determined by comparing the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are proteins and protein fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more, most preferably 30 or more) contiguous amino acids that shares at least 75% sequence identity (more preferably, at least 85% identity; most preferably at least 95% identity) with any such segment of any of the disclosed proteins.

In particular, sequence identity may be determined using WU-BLAST (Washington University BLAST) version 2.0 software, which builds upon WU-BLAST version 1.4, which in turn is based on the public domain NCBI-BLAST version 1.4 (Altschul and Gish, 1996, Local alignment statistics, Doolittle *ed.*, *Methods in Enzymology* **266**: 460-480; Altschul *et al.*, 1990, Basic local alignment search tool, *Journal of Molecular Biology* **215**: 403-410; Gish and States, 1993, Identification of protein coding regions by database similarity search, *Nature Genetics* **3**: 266-272; Karlin and Altschul, 1993, Applications and statistics for multiple high-scoring segments in molecular sequences, *Proc. Natl. Acad. Sci. USA* **90**: 5873-5877; all of which are incorporated by reference herein). WU-BLAST version 2.0 executable programs for several UNIX platforms can be downloaded from ftp://blast.wustl.edu/blast/executables. The complete suite of search programs (BLASTP, BLASTN, BLASTX, TBLASTN, and TBLASTX) is provided at that site, in addition to several support programs. WU-BLAST 2.0 is copyrighted and may not be sold or redistributed in any form or manner without the express written consent of the author; but the posted executables may otherwise be freely used for commercial, nonprofit, or academic purposes. In all search programs in the suite -- BLASTP, BLASTN, BLASTX, TBLASTN and TBLASTX -- the gapped alignment routines are integral to the database search itself, and thus yield much better sensitivity and selectivity while producing the more easily interpreted output. Gapping can optionally be turned off in all of these programs, if desired. The default penalty (Q) for a gap of length one is Q=9 for proteins

and BLASTP, and Q=10 for BLASTN, but may be changed to any integer value including zero, one through eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty, fifty-one through one hundred, etc. The default per-residue penalty for extending a gap (R) is R=2 for proteins and BLASTP, and R=10 for BLASTN, but may be changed to any integer value including zero, one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty, fifty-one through one hundred, etc. Any combination of values for Q and R can be used in order to align sequences so as to maximize overlap and identity while minimizing sequence gaps. The default amino acid comparison matrix is BLOSUM62, but other amino acid comparison matrices such as PAM can be utilized.

Species homologues of the disclosed polynucleotides and proteins are also provided by the present invention. As used herein, a "species homologue" is a protein or polynucleotide with a different species of origin from that of a given protein or polynucleotide, but with significant sequence similarity to the given protein or polynucleotide. Preferably, polynucleotide species homologues have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% identity) with the given polynucleotide, and protein species homologues have at least 30% sequence identity (more preferably, at least 45% identity; most preferably at least 60% identity) with the given protein, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides or the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Species homologues may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species. Preferably, species homologues are those isolated from mammalian species. Most preferably, species homologues are those isolated from certain mammalian species such as, for example, *Pan troglodytes*, *Gorilla gorilla*, *Pongo pygmaeus*, *Hylobates concolor*, *Macaca mulatta*, *Papio papio*, *Papio hamadryas*, *Cercopithecus aethiops*, *Cebus capucinus*, *Aotus trivirgatus*, *Sanguinus oedipus*, *Microcebus murinus*, *Mus musculus*, *Rattus norvegicus*, *Cricetulus griseus*, *Felis catus*, *Mustela vison*, *Canis familiaris*, *Oryctolagus cuniculus*, *Bos taurus*, *Ovis aries*, *Sus scrofa*, and *Equus caballus*, for which genetic maps have been created allowing the identification of syntenic relationships between the genomic organization of genes in one species and the genomic organization of the related genes in another species (O'Brien and Seuánez, 1988, *Ann. Rev. Genet.* **22**: 323-351; O'Brien *et al.*, 1993, *Nature Genetics* **3**:103-112; Johansson *et al.*, 1995, *Genomics* **25**: 682-690; Lyons *et al.*, 1997, *Nature Genetics* **15**: 47-56; O'Brien *et al.*, 1997, *Trends in Genetics* **13(10)**: 393-399; Carver and Stubbs, 1997, *Genome Research* **7**:1123-1137; all of which are incorporated by reference herein).

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotides which also encode proteins which are identical or have significantly similar sequences to those encoded by the disclosed polynucleotides. Preferably, allelic variants have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% identity) with the given polynucleotide, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps. Allelic variants may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from individuals of the appropriate species.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides that hybridize under reduced stringency conditions, more preferably stringent conditions, and most preferably highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in the table below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp)‡	Hybridization Temperature and Buffer†	Wash Temperature and Buffer†
A	DNA:DNA	≥ 50	65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
B	DNA:DNA	<50	T_B*; 1xSSC	T_B*; 1xSSC
C	DNA:RNA	≥ 50	67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
D	DNA:RNA	<50	T_D*; 1xSSC	T_D*; 1xSSC
E	RNA:RNA	≥ 50	70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
F	RNA:RNA	<50	T_F*; 1xSSC	T_F*; 1xSSC
G	DNA:DNA	≥ 50	65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
H	DNA:DNA	<50	T_H*; 4xSSC	T_H*; 4xSSC
I	DNA:RNA	≥ 50	67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
J	DNA:RNA	<50	T_J*; 4xSSC	T_J*; 4xSSC
K	RNA:RNA	≥ 50	70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
L	RNA:RNA	<50	T_L*; 2xSSC	T_L*; 2xSSC
M	DNA:DNA	≥ 50	50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
N	DNA:DNA	<50	T_N*; 6xSSC	T_N*; 6xSSC
O	DNA:RNA	≥ 50	55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
P	DNA:RNA	<50	T_P*; 6xSSC	T_P*; 6xSSC
Q	RNA:RNA	≥ 50	60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
R	RNA:RNA	<50	T_R*; 4xSSC	T_R*; 4xSSC

‡: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

†: SSPE (1xSSPE is 0.15M NaCl, 10mM NaH_2PO_4, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

*T_B - T_R: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, T_m(°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T_m(°C) = 81.5 + 16.6($\log_{10}$[Na^+]) + 0.41(%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na^+] is the concentration of sodium ions in the hybridization buffer ([Na^+] for 1xSSC = 0.165 M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory*

Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, each such hybridizing polynucleotide has a length that is at least 25%(more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps.

The isolated polynucleotide endcoing the protein of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman *et al.*, Nucleic Acids Res. 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, Methods in Enzymology 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from in vitro culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae, Schizosaccharomyces pombe, Kluyveromyces* strains, *Candida,* or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli, Bacillus subtilis, Salmonella typhimurium,* or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, California, U.S.A. (the MaxBac® kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl® or Cibacrom blue 3GA Sepharose®; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLabs (Beverly, MA), Pharmacia (Piscataway, NJ) and Invitrogen Corporation (Carlsbad, CA), respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from the Eastman Kodak Company (New Haven, CT).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and may thus be useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

Research Uses and Utilities

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding

protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, those described in Gyuris *et al.*, 1993, *Cell* 75: 791-803 and in Rossi *et al.*, 1997, *Proc. Natl. Acad. Sci. USA* 94: 8405-8410, all of which are incorporated by reference herein) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK. The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Bertagnolli, et al., J. Immunol. 149:3778-3783, 1992; Bowman et al., J. Immunol. 152: 1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon γ, Schreiber, R.D. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as

candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to regulate immune responses in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter

prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science *257*:789-792 (1992) and Turka *et al.*, Proc. Natl. Acad. Sci USA, *89*:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/*lpr*/*lpr* mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral

diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 microglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (*e.g.*, B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B

lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowmanet al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: *In vitro* antibody production, Mond, J.J. and Brunswick, M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology

67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow

transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 1-21, Wiley-Liss, Inc.., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H.J. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

Tissue Growth Activity

A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an

osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with

the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

Activin/Inhibin Activity

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin α family, may be useful as a contraceptive based on the ability of

inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin-β group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation,

those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in:Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Cadherin/Tumor Invasion Suppressor Activity

Cadherins are calcium-dependent adhesion molecules that appear to play major roles during development, particularly in defining specific cell types. Loss or alteration of normal cadherin expression can lead to changes in cell adhesion properties linked to tumor growth and metastasis. Cadherin malfunction is also implicated in other human diseases, such as pemphigus vulgaris and pemphigus foliaceus (auto-immune blistering skin diseases), Crohn's disease, and some developmental abnormalities.

The cadherin superfamily includes well over forty members, each with a distinct pattern of expression. All members of the superfamily have in common conserved extracellular repeats (cadherin domains), but structural differences are found in other parts of the molecule. The

cadherin domains bind calcium to form their tertiary structure and thus calcium is required to mediate their adhesion. Only a few amino acids in the first cadherin domain provide the basis for homophilic adhesion; modification of this recognition site can change the specificity of a cadherin so that instead of recognizing only itself, the mutant molecule can now also bind to a different cadherin. In addition, some cadherins engage in heterophilic adhesion with other cadherins.

E-cadherin, one member of the cadherin superfamily, is expressed in epithelial cell types. Pathologically, if E-cadherin expression is lost in a tumor, the malignant cells become invasive and the cancer metastasizes. Transfection of cancer cell lines with polynucleotides expressing E-cadherin has reversed cancer-associated changes by returning altered cell shapes to normal, restoring cells' adhesiveness to each other and to their substrate, decreasing the cell growth rate, and drastically reducing anchorage-independent cell growth. Thus, reintroducing E-cadherin expression reverts carcinomas to a less advanced stage. It is likely that other cadherins have the same invasion suppressor role in carcinomas derived from other tissue types. Therefore, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be used to treat cancer. Introducing such proteins or polynucleotides into cancer cells can reduce or eliminate the cancerous changes observed in these cells by providing normal cadherin expression.

Cancer cells have also been shown to express cadherins of a different tissue type than their origin, thus allowing these cells to invade and metastasize in a different tissue in the body. Proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be substituted in these cells for the inappropriately expressed cadherins, restoring normal cell adhesive properties and reducing or eliminating the tendency of the cells to metastasize.

Additionally, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can used to generate antibodies recognizing and binding to cadherins. Such antibodies can be used to block the adhesion of inappropriately expressed tumor-cell cadherins, preventing the cells from forming a tumor elsewhere. Such an anti-cadherin antibody can also be used as a marker for the grade, pathological type, and prognosis of a cancer, i.e. the more progressed the cancer, the less cadherin expression there will be, and this decrease in cadherin expression can be detected by the use of a cadherin-binding antibody.

Fragments of proteins of the present invention with cadherin activity, preferably a polypeptide comprising a decapeptide of the cadherin recognition site, and poly-nucleotides of the present invention encoding such protein fragments, can also be used to block cadherin function by binding to cadherins and preventing them from binding in ways that produce undesirable effects. Additionally, fragments of proteins of the present invention with cadherin activity,

preferably truncated soluble cadherin fragments which have been found to be stable in the circulation of cancer patients, and polynucleotides encoding such protein fragments, can be used to disturb proper cell-cell adhesion.

Assays for cadherin adhesive and invasive suppressor activity include, without limitation, those described in: Hortsch et al. J Biol Chem 270 (32): 18809-18817, 1995; Miyaki et al. Oncogene 11: 2547-2552, 1995; Ozawa et al. Cell 63: 1033-1038, 1990.

Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via antibody-dependent cell-mediated cytotoxicity (ADCC)). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or caricadic cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an

immune response against such protein or another material or entity which is cross-reactive with such protein.

ADMINISTRATION AND DOSING

A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a pharmaceutical composition when combined with a pharmaceutically acceptable carrier. Such a composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or compliment its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize side effects. Conversely, protein of the present invention may be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind

surface immunolgobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein by reference.

As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a mammal having a condition to be treated. Protein of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

Administration of protein of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous,

intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is administered orally, protein of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art.

The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μg

to about 100 mg (preferably about 0.1ng to about 10 mg, more preferably about 0.1 μg to about 1 mg) of protein of the present invention per kg body weight.

The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is contemplated that the duration of each application of the protein of the present invention will be in the range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

Protein of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. As used herein, the term "antibody" includes without limitation a polyclonal antibody, a monoclonal antibody, a chimeric antibody, a single-chain antibody, a CDR-grafted antibody, a humanized antibody, or fragments thereof which bind to the indicated protein. Such term also includes any other species derived from an antibody or antibody sequence which is capable of binding the indicated protein.

Antibodies to a particular protein can be produced by methods well known to those skilled in the art. For example, monoclonal antibodies can be produced by generation of antibody-producing hybridomas in accordance with known methods (see for example, Goding, 1983, Monoclonal antibodies: principles and practice, Academic Press Inc., New York; and Yokoyama, 1992, "Production of Monoclonal Antibodies" in Current Protocols in Immunology, Unit 2.5, Greene Publishing Assoc. and John Wiley & Sons). Polyclonal sera and antibodies can be produced by inoculation of a mammalian subject with the relevant protein or fragments thereof in accordance with known methods. Fragments of antibodies, receptors, or other reactive peptides can be produced from the corresponding antibodies by cleavage of and collection of the desired fragments in accordance with known methods (see for example, Goding, supra; and Andrew et al., 1992, "Fragmentation of Immunoglobulins" in Current Protocols in Immunology, Unit 2.8, Greene Publishing Assoc. and John Wiley & Sons). Chimeric antibodies and single chain antibodies can also be produced in accordance with known recombinant methods (see for example, 5,169,939, 5,194,594, and 5,576,184). Humanized antibodies can also be made from corresponding murine antibodies in accordance with well known methods (see for

example, U.S. Patent Nos. 5,530,101, 5,585,089, and 5,693,762). Additionally, human antibodies may be produced in non-human animals such as mice that have been genetically altered to express human antibody molecules (see for example Fishwild *et al.*, 1996, *Nature Biotechnology* **14**: 845-851; Mendez *et al.*, 1997, *Nature Genetics* **15**: 146-156 (erratum *Nature Genetics* **16**: 410); and U.S. Patents 5,877,397 and 5,625,126). Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R.P. Merrifield, J. Amer.Chem.Soc. 85, 2149-2154 (1963); J.L. Krstenansky, *et al.*, FEBS Lett. 211, 10 (1987).

Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium sulfate, tricalciumphosphate, hydroxyapatite,

polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorbtion of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF-α and TGF-β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins of the present invention.

The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue

(e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

Patent and literature references cited herein are incorporated by reference as if fully set forth.

What is claimed is:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:41;

(b) the nucleotide sequence of SEQ ID NO:41 from nucleotide 102 to nucleotide 2027;

(c) the nucleotide sequence of SEQ ID NO:41 from nucleotide 1902 to nucleotide 2027;

(d) the nucleotide sequence of SEQ ID NO:41 from nucleotide 1 to nucleotide 431;

(e) the nucleotide sequence of the full-length protein coding sequence of clone BG160_1 deposited with the ATCC under accession number 98232;

(f) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone BG160_1 deposited with the ATCC under accession number 98232;

(g) the nucleotide sequence of a mature protein coding sequence of clone BG160_1 deposited with the ATCC under accession number 98232;

(h) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone BG160_1 deposited with the ATCC under accession number 98232;

(i) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:42;

(j) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42;

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(h); and

(l) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(h), and that has a length that is at least 25% of the length of SEQ ID NO:41.

2. The polynucleotide of claim 1 wherein said polynucleotide is operably linked to at least one expression control sequence.

3. A host cell transformed with the polynucleotide of claim 2.

4. The host cell of claim 3, wherein said cell is a mammalian cell.

5. A process for producing a protein encoded by the polynucleotide of claim 2, which process comprises:

(a) growing a culture of a host cell in a suitable culture medium, wherein the host cell has been transformed with the polynucleotide of claim 2; and

(b) purifying said protein from the culture.

6. A protein produced according to the process of claim 5.

7. An isolated polynucleotide encoding the protein of claim 6.

8. The polynucleotide of claim 7, wherein the polynucleotide comprises the cDNA insert of clone BG160_1 deposited with the ATCC under accession number 98232.

9. A protein comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:42;

(b) the amino acid sequence of SEQ ID NO:42 from amino acid 1 to amino acid 110;

(c) a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42; and

(d) the amino acid sequence encoded by the cDNA insert of clone BG160_1 deposited with the ATCC under accession number 98232;

the protein being substantially free from other mammalian proteins.

10. The protein of claim 9, wherein said protein comprises the amino acid sequence of SEQ ID NO:42.

11. A composition comprising the protein of claim 9 and a pharmaceutically acceptable carrier.

12. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:129;

(b) the nucleotide sequence of SEQ ID NO:129 from nucleotide 383 to nucleotide 3958;

(c) the nucleotide sequence of SEQ ID NO:129 from nucleotide 470 to nucleotide 3958;

(d) the nucleotide sequence of SEQ ID NO:129 from nucleotide 271 to nucleotide 488;

(e) the nucleotide sequence of the full-length protein coding sequence of clone CO722_1 deposited with the ATCC under accession number 98271;

(f) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone CO722_1 deposited with the ATCC under accession number 98271;

(g) the nucleotide sequence of a mature protein coding sequence of clone CO722_1 deposited with the ATCC under accession number 98271;

(h) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone CO722_1 deposited with the ATCC under accession number 98271;

(i) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:130;

(j) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130, the fragment comprising eight contiguous amino acids of SEQ ID NO:130;

(k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(h); and

(l) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(h), and that has a length that is at least 25% of the length of SEQ ID NO:129.

13. A protein comprising an amino acid sequence selected from the group consisting of:

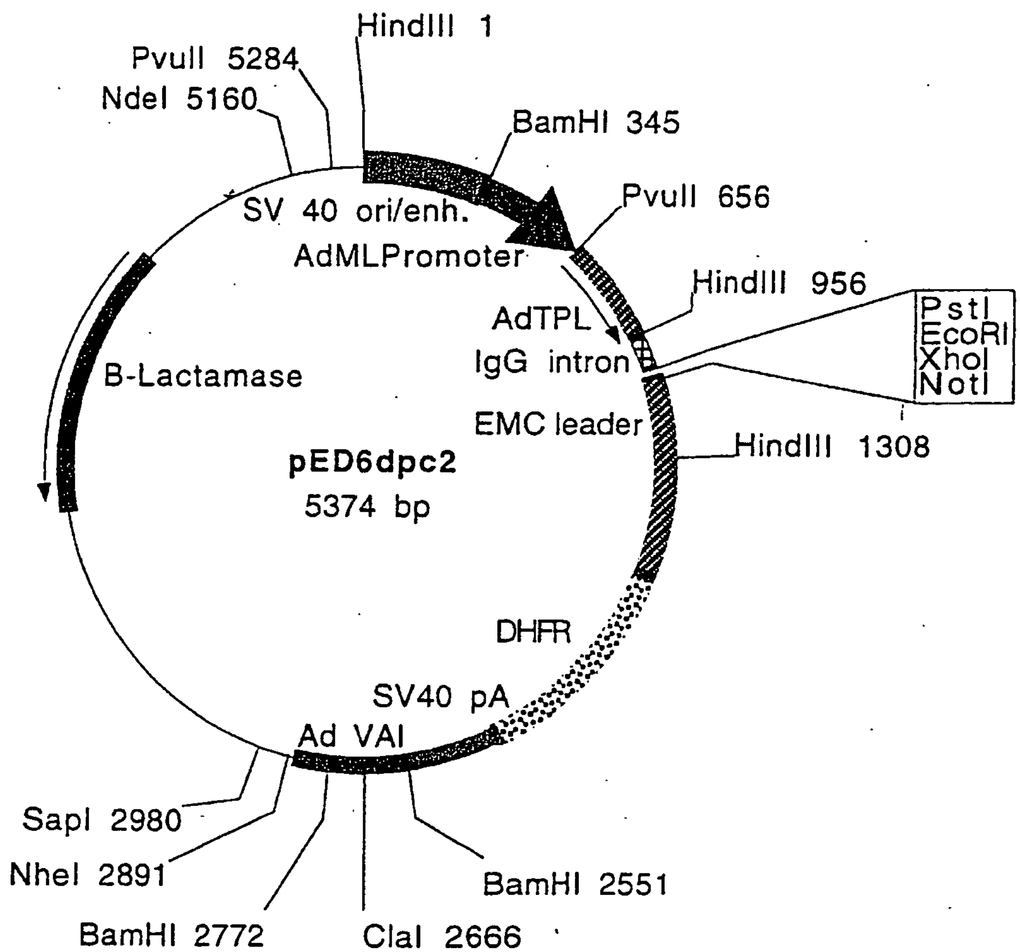
(a) the amino acid sequence of SEQ ID NO:130;

(b) the amino acid sequence of SEQ ID NO:130 from amino acid 1 to amino acid 34;

(c) a fragment of the amino acid sequence of SEQ ID NO:130, the fragment comprising eight contiguous amino acids of SEQ ID NO:130; and

(d) the amino acid sequence encoded by the cDNA insert of clone CO722_1 deposited with the ATCC under accession number 98271;

the protein being substantially free from other mammalian proteins.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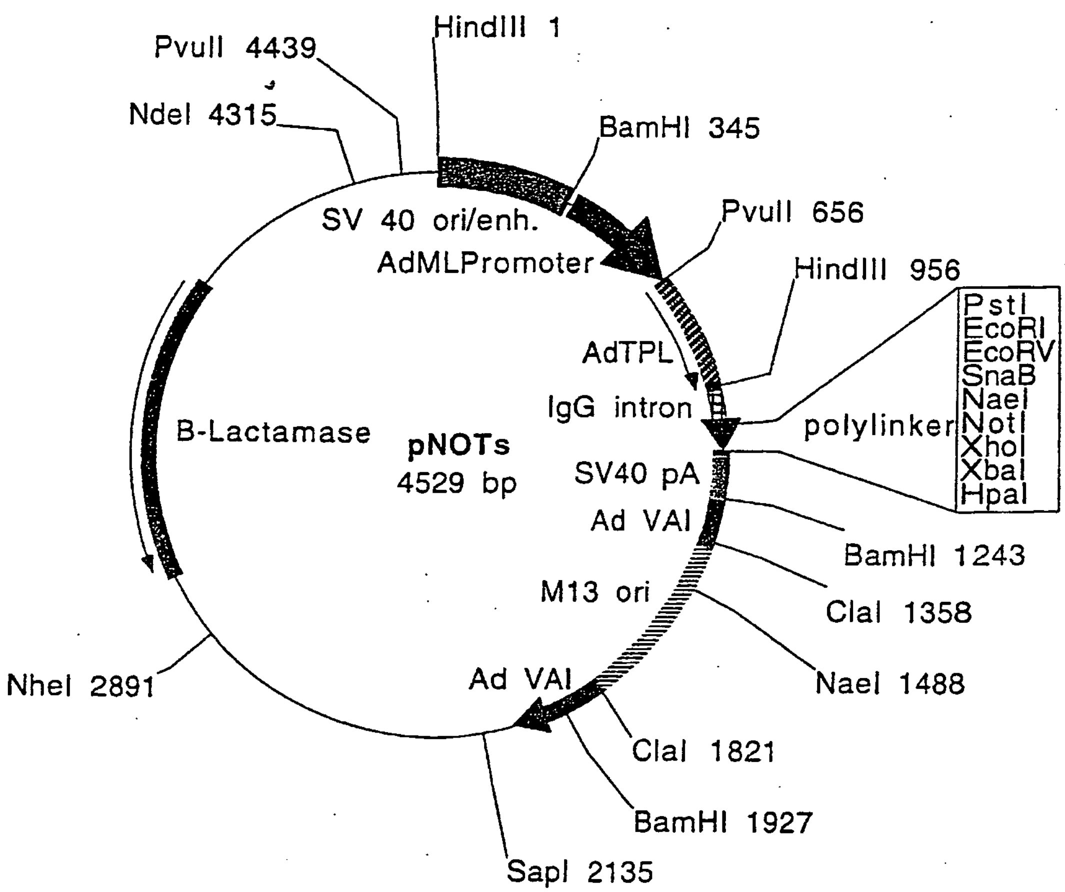
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<212> PRT

<213> Homo sapiens

<220>
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Leu Asp His Gln Arg Gln Ala Ser Arg Thr Pro Cys Pro Arg Pro Pro
35 40 45

Leu Ala Gly Thr Gln Gly Leu Val Thr Asp Thr Arg Ala Ala Pro Leu
50 55 60

Thr Pro Ile Gly Thr Pro Leu Pro Ser Ala Ile Pro Ser Gly Tyr Cys
65 70 75 80

Ser Gln Asp Gly Gln Thr Gly Arg Gln Pro Leu Pro Pro Tyr Thr Pro
85 90 95

Ala Met Met His Arg Ser Asn Gly His Thr Leu Thr Gln Pro Pro Gly
100 105 110

Pro Arg Gly Cys Glu Gly Asp Gly Pro Glu His Gly Val Glu Glu Gly
115 120 125

Thr Arg Lys Arg Val Ser Leu Pro Gln Trp Pro Pro Pro Ser Arg Ala
130 135 140

Lys Trp Ala His Ala Ala Arg Glu Asp Ser Leu Pro Glu Glu Ser Ser
145 150 155 160

Ala Pro Asp Phe Ala Asn Leu Lys His Tyr Gln Lys Gln Gln Ser Leu
165 170 175

Pro Ser Leu Cys Ser Thr Ser Asp Pro Asp Thr Pro Leu Gly Ala Pro
180 185 190

Ser Thr Pro Gly Arg Ile Ser Leu Arg Ile Ser Glu Ser Val Leu Arg
195 200 205

Asp Ser Pro Pro Pro His Glu Asp Tyr Glu Asp Glu Val Phe Val Arg
210 215 220

Asp Pro His Pro Lys Ala Thr Ser Ser Pro Thr Phe Glu Pro Leu Pro
225 230 235 240

Pro Pro Pro Pro Pro Pro Pro Ser Gln Glu Thr Pro Val Tyr Xaa Met
245 250 255

Asp Asp Phe Pro Pro Pro Pro Pro His Thr Val Cys Glu Ala Gln Leu
260 265 270

Asp Ser Glu Asp Pro Glu Gly Pro Arg Pro Ser Phe Asn Lys Leu Ser
275 280 285

Lys Val Thr Ile Ala Arg Glu Arg His Met Pro Gly Ala Ala His Val
290 295 300

Val Gly Ser Gln Thr Leu Ala Ser Arg Leu Gln Thr Ser Ile Lys Gly
305 310 315 320

Ser Glu Ala Glu Ser Thr Pro Pro Ser Phe Met Ser Val His Ala Gln
325 330 335

Leu Ala Gly Ser Leu Gly Gly Gln Pro Ala Pro Ile Gln Thr Gln Ser
340 345 350

Leu Ser His Asp Pro Val Ser Gly Thr Gln Gly Leu Glu Lys Lys Val
355 360 365

Ser Pro Asp Pro Gln Lys Ser Ser Glu Asp Ile Arg Thr Glu Ala Leu
370 375 380

Ala Lys Glu Ile Val His Gln Asp Lys Ser Leu Ala Asp Ile Leu Asp
385 390 395 400

Pro Asp Ser Arg Leu Lys Thr Thr Met Asp Leu Met Glu Gly Leu Phe
405 410 415

Pro Arg Asp Val Asn Leu Leu Lys Glu Asn Ser Val Lys Arg Lys Ala
420 425 430

Ile Gln Arg Thr Val Ser Ser Ser Gly Cys Glu Gly Lys Arg Asn Glu
435 440 445

Asp Lys Glu Ala Val Ser Met Leu Val Asn Cys Pro Ala Tyr Tyr Ser
450 455 460

Val Ser Ala Pro Lys Ala Glu Leu Leu Asn Lys Ile Lys Glu Met Pro
465 470 475 480

Ala Glu Val Asn Glu Glu Glu Glu Gln Ala Asp Val Asn Glu Lys Lys
485 490 495

Ala Glu Leu Ile Gly Ser Leu Thr His Lys Leu Glu Thr Leu Gln Glu
500 505 510

Ala Lys Gly Ser Leu Leu Thr Asp Ile Lys Leu Asn Asn Ala Leu Gly
515 520 525

Glu Glu Val Glu Ala Leu Ile Ser Glu Leu Cys Lys Pro Asn Glu Phe
530 535 540

Asp Lys Tyr Arg Met Phe Ile Gly Asp Leu Asp Lys Val Val Asn Leu
545 550 555 560

Leu Leu Ser Leu Ser Gly Arg Leu Ala Arg Val Glu Asn Val Leu Ser
565 570 575

Gly Leu Gly Glu Asp Ala Ser Asn Glu Glu Arg Ser Ser Leu Tyr Glu
580 585 590

Lys Arg Lys Ile Leu Ala Gly Gln His Glu Asp Ala Arg Glu Leu Lys
595 600 605

Glu Asn Leu Asp Arg Arg Glu Arg Val Val Leu Gly Ile Leu Ala Asn
610 615 620

Tyr Leu Ser Glu Glu Gln Leu Gln Asp Tyr Gln His Phe Val Lys Met
625 630 635 640

Lys Ser Thr Leu Leu Ile Glu Gln Arg Lys Leu Asp Asp Lys Ile Lys
645 650 655

Leu Gly Gln Glu Gln Val Lys Cys Leu Leu Glu Ser Leu Pro Ser Asp
660 665 670

Phe Ile Pro Lys Ala Gly Ala Leu Ala Leu Pro Pro Asn Leu Thr Ser
675 680 685

Glu Pro Ile Pro Ala Gly Gly Cys Thr Phe Ser Gly Ile Phe Pro Thr
690 695 700

Leu Thr Ser Pro Leu
705

<210> 6
<211> 190
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (4)

<220>
<221> unsure
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actcagagtg gaaatcttgt ccacagctac cgangcactg gcggcatctt ccangtgtgc 180
tggaacgccc 190

<210> 7
<211> 391
<212> DNA
<213> Homo sapiens

<400> 7

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cccaatgaac aaagaagatt ttagaaaata gaaagctgtt gggattacaa agttgcgcgt 180
ttcatcggta caaactggtc tttgaacctc ctttgtgaga gcaattgtag tgtccaaatt 240
gttagggaaa acaaaaaaaa aaaatcccaa ggaggagggt ttttcccccct tccctgtttg 300
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<210> 8
<211> 62
<212> PRT
<213> Homo sapiens

<400> 8
Thr Ser Phe Val Arg Ala Ile Val Val Ser Lys Leu Leu Gly Lys Thr
1   5   10   15

Lys Lys Lys Asn Pro Lys Glu Glu Gly Phe Ser Pro Phe Pro Val Trp
            20   25   30

Phe Ile Thr Ala Phe Cys Phe Phe Phe Gly Thr Ala Phe Tyr Val Ser
        35   40   45

Phe His Ser Ala Ile Thr Glu Pro Val Pro Gly Gly Asn Gln
    50   55   60

<210> 9
<211> 267
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (21)

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agaaaaaaaa atgacttata agagaaagag cctggagtat ttttggaaaa aaaaataata 180
tttttatgtt aaaacaattt taaatcttta aaatggccat cagacataga gagctttgtg 240
tgattcatgt tttaaaaaaa aaaaaaa 267

<210> 10
<211> 2178
<212> DNA
<213> Homo sapiens

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gaatgctact gtgtacttac aaaccacact catattcgtc acgtcatttc atcttcaccc 180
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<210> 11
<211> 487
<212> PRT
<213> Homo sapiens

<400> 11

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Leu Val Gln Leu Ala Ala Arg Leu Arg Pro Ala Leu Cys Asp Thr Leu
            20                  25                  30

Ile Thr Val Gly Ser Gln Glu Phe Pro Ala His Ser Leu Val Leu Ala
        35                  40                  45

Gly Val Ser Gln Gln Leu Gly Arg Arg Gly Gln Trp Ala Leu Gly Glu
    50                  55                  60

Gly Ile Ser Pro Ser Thr Phe Ala Gln Leu Leu Asn Phe Val Tyr Gly
65                  70                  75                  80

Glu Ser Val Glu Leu Gln Pro Gly Glu Leu Arg Pro Leu Gln Glu Ala
                85                  90                  95

Ala Arg Ala Leu Gly Val Gln Ser Leu Glu Glu Ala Cys Trp Arg Ala
            100                 105                 110

Arg Gly Asp Arg Ala Lys Lys Pro Asp Pro Gly Leu Lys Lys His Gln
        115                 120                 125

Glu Glu Pro Glu Lys Pro Ser Arg Asn Pro Glu Arg Glu Leu Gly Asp
    130                 135                 140
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Pro Gly Glu Lys Gln Lys Pro Glu Gln Val Ser Arg Thr Gly Gly Arg
145 150 155 160

Glu Gln Glu Met Leu His Lys His Ser Pro Pro Arg Gly Arg Pro Glu
165 170 175

Met Ala Gly Ala Thr Gln Glu Ala Gln Gln Glu Gln Thr Arg Ser Lys
180 185 190

Glu Lys Arg Leu Gln Ala Pro Val Gly Gln Arg Gly Ala Asp Gly Lys
195 200 205

His Gly Val Leu Thr Trp Leu Arg Glu Asn Pro Gly Gly Ser Glu Glu
210 215 220

Ser Leu Arg Lys Leu Pro Gly Pro Leu Pro Pro Ala Gly Ser Leu Gln
225 230 235 240

Thr Ser Val Thr Pro Arg Pro Ser Trp Ala Glu Ala Pro Trp Leu Val
245 250 255

Gly Gly Gln Pro Ala Leu Trp Ser Ile Leu Leu Met Pro Pro Arg Tyr
260 265 270

Gly Ile Pro Phe Tyr His Ser Thr Pro Thr Thr Gly Ala Trp Gln Glu
275 280 285

Val Trp Arg Glu Gln Arg Ile Pro Leu Ser Leu Asn Ala Pro Lys Gly
290 295 300

Leu Trp Ser Gln Asn Gln Leu Ala Ser Ser Ser Pro Thr Pro Gly Ser
305 310 315 320

Leu Pro Gln Gly Pro Ala Gln Leu Ser Pro Gly Glu Met Glu Glu Ser
325 330 335

Asp Gln Gly His Thr Gly Ala Leu Ala Thr Cys Ala Gly His Glu Asp
340 345 350

Lys Ala Gly Cys Pro Pro Arg Pro His Pro Pro Pro Ala Pro Pro Ala
355 360 365

Arg Ser Arg Pro Tyr Ala Cys Ser Val Cys Gly Lys Arg Phe Ser Leu
370 375 380

Lys His Gln Met Glu Thr His Tyr Arg Val His Thr Gly Glu Lys Pro
385 390 395 400

Phe Ser Cys Ser Leu Cys Pro Gln Arg Ser Arg Asp Phe Ser Ala Met
405 410 415

Thr Lys His Leu Arg Thr His Gly Ala Ala Pro Tyr Arg Cys Ser Leu
420 425 430

Cys Gly Ala Gly Cys Pro Ser Leu Ala Ser Met Gln Ala His Met Arg
435 440 445

Gly His Ser Pro Ser Gln Leu Pro Pro Gly Trp Thr Ile Arg Ser Thr
450 455 460

Phe Leu Tyr Ser Ser Ser Arg Pro Ser Arg Pro Ser Thr Ser Pro Cys
465 470 475 480

Cys Pro Ser Ser Ser Thr Thr
485

<210> 12
<211> 2436
<212> DNA
<213> Homo sapiens

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<210> 13
<211> 763
<212> PRT
<213> Homo sapiens

<400> 13

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Leu Trp Asp Tyr Ile Asp Gly Ile Leu Ile Lys Thr Phe Ile Val Gly
            20   25   30

Cys Lys Leu His Ala Leu Phe Thr Leu Ala Gln Ala Glu Asp Ser Val
        35   40   45

Phe Val Ile Val Asn Lys Glu Lys Pro Asp Ile Phe Gln Leu Val Ser
    50   55   60

Val Lys Leu Pro Lys Ser Ser Ser Gln Glu Val Glu Ala Lys Glu Leu
65   70   75   80

Ser Phe Val Leu Asp Tyr Ile Asn Gln Ser Pro Lys Cys Ile Ala Phe
                85   90   95

Gly Asn Glu Gly Val Tyr Val Ala Ala Val Arg Glu Phe Tyr Leu Ser
            100   105   110

Val Tyr Phe Phe Lys Lys Lys Thr Thr Ser Arg Phe Thr Leu Ser Ser
        115   120   125

Ser Arg Asn Lys Lys His Ala Lys Asn Asn Phe Thr Cys Val Ala Cys
    130   135   140

His Pro Thr Glu Asp Cys Ile Ala Ser Gly His Met Asp Gly Lys Ile
145   150   155   160

Arg Leu Trp Arg Asn Phe Tyr Asp Asp Lys Lys Tyr Thr Tyr Thr Cys
                165   170   175

Leu His Trp His His Asp Met Val Met Asp Leu Ala Phe Ser Val Thr
            180   185   190

Gly Thr Ser Leu Leu Ser Gly Gly Arg Glu Ser Val Leu Val Glu Trp
        195   200   205

Arg Asp Ala Thr Glu Lys Asn Lys Glu Phe Leu Pro Arg Leu Gly Ala
    210   215   220

Thr Ile Glu His Ile Ser Val Ser Pro Ala Gly Asp Leu Phe Cys Thr
225   230   235   240

Ser His Ser Asp Asn Lys Ile Ile Ile Ile His Arg Asn Leu Glu Ala
                245   250   255

Ser Ala Val Ile Gln Gly Leu Val Lys Asp Arg Ser Ile Phe Thr Gly
            260   265   270

Leu Met Ile Asp Pro Arg Thr Lys Ala Leu Val Leu Asn Gly Lys Pro
        275   280   285

Gly His Leu Gln Phe Tyr Ser Leu Gln Ser Asp Lys Gln Leu Tyr Asn
    290   295   300

Leu Asp Ile Ile Gln Gln Glu Tyr Ile Asn Asp Tyr Gly Leu Ile Gln
305   310   315   320

Ile Glu Leu Thr Lys Ala Ala Phe Gly Cys Phe Gly Asn Trp Leu Ala
325 330 335

Thr Val Glu Gln Arg Gln Glu Lys Glu Thr Glu Leu Glu Leu Gln Met
340 345 350

Lys Leu Trp Met Tyr Asn Lys Lys Thr Gln Gly Phe Ile Leu Asn Thr
355 360 365

Lys Ile Asn Met Pro His Glu Asp Cys Ile Thr Ala Leu Cys Phe Cys
370 375 380

Asn Ala Glu Lys Ser Glu Gln Pro Thr Leu Val Thr Ala Ser Lys Asp
385 390 395 400

Gly Tyr Phe Lys Val Trp Ile Leu Thr Asp Asp Ser Asp Ile Tyr Lys
405 410 415

Lys Ala Val Gly Trp Thr Cys Asp Phe Val Gly Ser Tyr His Lys Tyr
420 425 430

Gln Ala Thr Asn Cys Cys Phe Ser Glu Asp Gly Ser Leu Leu Ala Val
435 440 445

Ser Phe Glu Glu Ile Val Thr Ile Trp Asp Ser Val Thr Trp Glu Leu
450 455 460

Lys Cys Thr Phe Cys Gln Arg Ala Gly Lys Ile Arg His Leu Cys Phe
465 470 475 480

Gly Arg Leu Thr Cys Ser Lys Tyr Leu Leu Gly Ala Thr Glu Asn Gly
485 490 495

Ile Leu Cys Cys Trp Asn Leu Leu Ser Cys Ala Leu Glu Trp Asn Ala
500 505 510

Lys Leu Asn Val Arg Val Met Glu Pro Asp Pro Asn Ser Glu Asn Ile
515 520 525

Ala Ala Ile Ser Gln Ser Ser Val Gly Ser Asp Leu Phe Val Phe Lys
530 535 540

Pro Ser Glu Pro Arg Pro Leu Tyr Ile Gln Lys Gly Ile Ser Arg Glu
545 550 555 560

Lys Val Gln Trp Gly Val Phe Val Pro Arg Asp Val Pro Glu Ser Phe
565 570 575

Thr Ser Glu Ala Tyr Gln Trp Leu Asn Arg Ser Gln Phe Tyr Phe Leu
580 585 590

Thr Lys Ser Gln Ser Leu Leu Thr Phe Ser Thr Lys Ser Pro Glu Glu
595 600 605

Lys Leu Thr Pro Thr Ser Lys Gln Leu Leu Ala Glu Glu Ser Leu Pro
610 615 620

Thr Thr Pro Phe Tyr Phe Ile Leu Gly Lys His Arg Gln Gln Gln Asp
625 630 635 640

Glu Lys Leu Asn Glu Thr Leu Glu Asn Glu Leu Val Gln Leu Pro Leu
645 650 655

Thr Glu Asn Ile Pro Ala Ile Ser Glu Leu Leu His Thr Pro Ala His
660 665 670

Val Leu Pro Ser Ala Ala Phe Leu Cys Ser Met Phe Val Asn Ser Leu
675 680 685

Leu Leu Ser Lys Glu Thr Lys Ser Ala Lys Glu Ile Pro Glu Asp Val
690 695 700

Asp Met Glu Glu Glu Lys Glu Ser Glu Asp Ser Asp Glu Glu Asn Asp
705 710 715 720

Phe Thr Glu Lys Val Gln Asp Thr Ser Asn Thr Gly Leu Gly Glu Asp
725 730 735

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<400> 19

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Pro Pro Glu Ser Gln Gln Val Arg Trp Glu Lys Gln Gln Pro Thr Pro
        35                  40                  45

Arg Leu Thr Leu Arg Asp Leu Gln Asn Lys Ser Ser Ser Cys Ser Ser
    50                  55                  60

Pro Ser Ser Ser Ala Thr Ser Leu Leu His Thr Val Ser Pro Glu Pro
65                  70                  75                  80

Pro Arg Pro Pro Gln Gln Pro Val Pro Thr Glu Leu Ser Leu Ala Ser
                85                  90                  95

Ile Thr Val Pro Leu Glu Ser Ile Lys Pro Ser Asn Ile Leu Pro Val
            100                 105                 110

Thr Val Tyr Asp Gln His Gly Phe Arg Ile Leu Phe His Phe Ala Arg
        115                 120                 125

Asp Pro Leu Pro Gly Arg Ser Asp Val Leu Val Val Val Val Ser Met
    130                 135                 140

Leu Ser Thr Ala Pro Gln Pro Ile Arg Asn Ile Val Phe Gln Ser Ala
145                 150                 155                 160

Val Pro Lys Val Met Lys Val Lys Leu Gln Pro Pro Ser Gly Thr Glu
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Leu Pro Ala Phe Asn Pro Ile Val His Pro Ser Ala Ile Thr Gln Val
180 185 190

Leu Leu Leu Ala Asn Pro Gln Lys Glu Lys Val Arg Leu Arg Tyr Lys
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Leu Thr Phe Thr Met Gly Asp Gln Thr Tyr Asn Glu Met Gly Asp Val
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Asp Gln Phe Pro Pro Pro Glu Thr Trp Gly Ser Leu
225 230 235

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<213> Homo sapiens

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Asn Ile Val Thr Ala Glu Val His Trp Ala Asn Leu Thr Val Ser Glu
35 40 45

Cys Gln Glu Met His Gly Glu Phe Met Gly Ser Ala Cys Gly His His
50 55 60

Gly Pro Tyr Thr Pro Asp Val Leu Phe Trp Ser Cys Ile Leu Phe Phe
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Thr Thr Phe Ile Leu Ser Ser
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             20                  25                  30

Leu Tyr Ala Ala Ser Ser Ile Lys Ser Asn Tyr Leu Val Phe Met Ala
         35                  40                  45

Glu Leu Phe Trp Trp Phe Glu Val Val Lys Pro Ser Phe Val Gln Pro
     50                  55                  60

Arg Val Val Arg Pro Gln Gly Ala Glu Pro Val Lys Asp Met Pro Ser
 65                  70                  75                  80

Ile Pro Val Leu Asn Ala Ala Lys Arg Asn Val Leu Asp Ser Ser Ser
                 85                  90                  95

Asp Phe Pro Ser Ser Gly Glu Gly Ala Thr Phe Thr Gln Ser His Leu
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<212> PRT
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Phe Gln Phe Leu His Asp Leu Ala Pro Thr Thr Cys Leu Thr Val Phe
20 25 30

Pro Thr Thr Leu Leu Pro Phe Leu Leu Leu Ile Asn Thr Gly Leu Met
35 40 45

Val Phe Pro Leu Thr Cys Gln Ala Cys Leu Thr Leu Ser Cys Leu Arg
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<210> 29
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<212> DNA
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35 40 45

Ser Leu Thr Thr Glu Asp Asp Thr Lys Leu Asn Pro Tyr Ala Gly Gly
50 55 60

Asp Gly Leu Gln Asn Asn Leu Ser Pro Lys Thr Lys Gly Thr Pro Val
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His Leu Gly Thr Ile Val Gly Ile Val Leu Ala Val Leu Leu Val Ala
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<212> DNA
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aaaaaa 3906

<210> 33
<211> 286
<212> PRT
<213> Homo sapiens

<400> 33
Met Lys Cys Ser Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn
1   5   10   15

Tyr Thr Leu Tyr Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys
            20   25   30

Glu Asn Ile Phe Arg Glu Gly Gln Tyr Leu Gly Cys Ser Phe Asp Leu
        35   40   45

Thr Lys Val Lys Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile Met
    50   55   60

Val Lys Asp Asn Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val Pro
65   70   75   80

Leu Thr Ser Arg Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu Ser

85 90 95

Phe His Asn Asp Asp Leu Tyr Val Gln Trp Glu Asn Pro Gln Asn Phe
100 105 110

Ile Ser Arg Cys Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln Thr
115 120 125

Glu Thr His Asn Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro
130 135 140

Glu Phe Glu Arg Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro Gly
145 150 155 160

Val Leu Pro Asp Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn
165 170 175

Lys Leu Cys Tyr Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu
180 185 190

Met Ser Ile Gly Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu
195 200 205

Leu Ile Val Pro Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu Leu
210 215 220

Tyr Leu Lys Arg Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro
225 230 235 240

Gly Lys Ile Phe Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu
245 250 255

His Trp Lys Lys Tyr Asp Ile Tyr Glu Lys Gln Thr Lys Glu Glu Thr
260 265 270

Asp Ser Val Val Leu Ile Glu Asn Leu Lys Lys Ala Ser Gln
275 280 285

<210> 34
<211> 1605
<212> DNA
<213> Homo sapiens

<400> 34
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aagatgttta cagagaccct tctccctgtg cagttaggag tgtaaggcaa gagagcccct 180
acttcatggg gcagatcaag agctgagacc aaagatggtc tatgttgctg accttgtcct 240
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gcacttcctg acgttgctgg tagtgcctgc catcaagaaa gattatggtt cccaggaaga 840
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caaaatgcat aaacctgtta caatgttgaa aaaaaaaaa aaaaa                  1605

<210> 35
<211> 241
<212> PRT
<213> Homo sapiens

<400> 35
Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu
1               5                   10                  15

Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val
            20                  25                  30

Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser
        35                  40                  45

Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly
    50                  55                  60

Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr
65                  70                  75                  80

Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile
                85                  90                  95

Phe Ile Ala Glu Val Ala Ala Ala Val Val Ala Leu Val Tyr Thr Thr
            100                 105                 110

Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys
        115                 120                 125

Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met
    130                 135                 140

Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp
145                 150                 155                 160

Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn
                165                 170                 175

Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala
            180                 185                 190

His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile
        195                 200                 205

Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly
    210                 215                 220
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Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu
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Gln

<210> 36
<211> 377
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (346)

<400> 36
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tcagggaaca ccagcatccc gagggttctt cgcagctgcc atcctcttcc tatcacagtc 240
ccacgtggcg cgggccaccc cgggctcaga ccaggcagtg ctagccctgt cccctgagta 300
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<210> 37
<211> 106
<212> PRT
<213> Homo sapiens

<220>
<221> UNSURE
<222> (96)

<400> 37
Met Asn Thr Leu Met Thr Ser Leu Pro Ala Leu Val Gln Gln Gln Gly
1 5 10 15

Arg Leu Leu Leu Ala Ala Asn Val Ala Thr Leu Gly Leu Leu Met Ala
20 25 30

Arg Leu Leu Ser Thr Ser Pro Ala Leu Gln Gly Thr Pro Ala Ser Arg
35 40 45

Gly Phe Phe Ala Ala Ala Ile Leu Phe Leu Ser Gln Ser His Val Ala
50 55 60

Arg Ala Thr Pro Gly Ser Asp Gln Ala Val Leu Ala Leu Ser Pro Glu
65 70 75 80

Tyr Glu Gly Ile Trp Ala Asp Leu Gln Glu Leu Trp Phe Leu Gly Xaa
85 90 95

Gln Ala Phe Thr Gly Cys Val Pro Leu Leu
100 105

<210> 38
<211> 245

<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (3)

<220>
<221> unsure
<222> (17)

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<221> unsure
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<222> (46)

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<220>
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<220>
<221> unsure
<222> (214)

<400> 38
tangactcct ctctgcngag acgcgactgg cggntccagc agggantacc ttttttataa 60
acccnggggg nccacacaca cacacacaca cacacacaca cacacacaca cacacacaca 120
catttttgat cccttgcttc cntcccccag tgcgttctgt gatcgccaag ttcaaagctg 180
tgcacatgtg gacactcaat aaatgttcat tggngacaaa aaaaaaaaaa aaaaaaaaaa 240
aaaaa 245

<210> 39
<211> 2384
<212> DNA
<213> Homo sapiens

<400> 39
ccaaaacatg ctcaaaagta gaacattttg tttcaatatt aggaaagtgc tttgaatccc 60
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gaataacagg tgcccagact ctaccaaagc atgtttctac cagcagtgat gaagggagcc 180
ccagtgccag tacaccaatg atcaataaaa ctggctttaa attttcagct gagaagcctg 240
tgattgaagt tcccagcatg acaatcctgg ataaaaagga tggagagcag gccaaagccc 300
tgtttgagaa agtgaggaag ttccgtgccc atgtggaaga tagtgacttg atctataaac 360
tctatgtggt ccaaacagtt atcaaaacag ccaagttcat ttttattctc tgctatacag 420
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tcagttacat atccattatt tgtgtttatg gctttatctg cctctacact ctcttctggt 600
tattcaggat acctttgaag gaatattctt tcgaaaaagt cagagaagag agcagtttta 660
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aagtaaatga ttaaattgac attttcttac tataaaaaaa aaaa 2384

<210> 40
<211> 614
<212> PRT
<213> Homo sapiens

<220>
<221> UNSURE
<222> (607)

<400> 40
Met Ile Asn Lys Thr Gly Phe Lys Phe Ser Ala Glu Lys Pro Val Ile
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Glu Val Pro Ser Met Thr Ile Leu Asp Lys Lys Asp Gly Glu Gln Ala
20 25 30

Lys Ala Leu Phe Glu Lys Val Arg Lys Phe Arg Ala His Val Glu Asp
35 40 45

Ser Asp Leu Ile Tyr Lys Leu Tyr Val Val Gln Thr Val Ile Lys Thr
50 55 60

Ala Lys Phe Ile Phe Ile Leu Cys Tyr Thr Ala Asn Phe Val Asn Ala
65 70 75 80

Ile Ser Phe Glu His Val Cys Lys Pro Lys Val Glu His Leu Ile Gly
85 90 95

Tyr Glu Val Phe Glu Cys Thr His Asn Met Ala Tyr Met Leu Lys Lys
100 105 110

Leu Leu Ile Ser Tyr Ile Ser Ile Ile Cys Val Tyr Gly Phe Ile Cys
115 120 125

Leu Tyr Thr Leu Phe Trp Leu Phe Arg Ile Pro Leu Lys Glu Tyr Ser
130 135 140

Phe Glu Lys Val Arg Glu Glu Ser Ser Phe Ser Asp Ile Pro Asp Val
145 150 155 160

Lys Asn Asp Phe Ala Phe Leu Leu His Met Val Asp Gln Tyr Asp Gln
165 170 175

Leu Tyr Ser Lys Arg Phe Gly Val Phe Leu Ser Glu Val Ser Glu Asn
180 185 190

Lys Leu Arg Glu Ile Ser Leu Asn His Glu Trp Thr Phe Glu Lys Leu
195 200 205

Arg Gln His Ile Ser Arg Asn Ala Gln Asp Lys Gln Glu Leu His Leu
210 215 220

Phe Met Leu Ser Gly Val Pro Asp Ala Val Phe Asp Leu Thr Asp Leu
225 230 235 240

Asp Val Leu Lys Leu Glu Leu Ile Pro Glu Ala Lys Ile Pro Ala Lys
245 250 255

Ile Ser Gln Met Thr Asn Leu Gln Glu Leu His Leu Cys His Cys Pro
260 265 270

Ala Lys Val Glu Gln Thr Ala Phe Ser Phe Leu Arg Asp His Leu Arg
275 280 285

Cys Leu His Val Lys Phe Thr Asp Val Ala Glu Ile Pro Ala Trp Val
290 295 300

Tyr Leu Leu Lys Asn Leu Arg Glu Leu Tyr Leu Ile Gly Asn Leu Asn
305 310 315 320

Ser Glu Asn Asn Lys Met Ile Gly Leu Glu Ser Leu Arg Glu Leu Arg
325 330 335

His Leu Lys Ile Leu His Val Lys Ser Asn Leu Thr Lys Val Pro Ser
340 345 350

Asn Ile Thr Asp Val Ala Pro His Leu Thr Lys Leu Val Ile His Asn
355 360 365

Asp Gly Thr Lys Leu Leu Val Leu Asn Ser Leu Lys Lys Met Met Asn
370 375 380

Val Ala Glu Leu Glu Leu Gln Asn Cys Glu Leu Glu Arg Ile Pro His
385 390 395 400

Ala Ile Phe Ser Leu Ser Asn Leu Gln Glu Leu Asp Leu Lys Ser Asn
405 410 415

Asn Ile Arg Thr Ile Glu Glu Ile Ile Ser Phe Gln His Leu Lys Arg
420 425 430

Leu Thr Cys Leu Lys Leu Trp His Asn Lys Ile Val Thr Ile Pro Pro
435 440 445

Ser Ile Thr His Val Lys Asn Leu Glu Ser Leu Tyr Phe Ser Asn Asn
450 455 460

Lys Leu Glu Ser Leu Pro Val Ala Val Phe Ser Leu Gln Lys Leu Arg
465 470 475 480

Cys Leu Asp Val Ser Tyr Asn Asn Ile Ser Met Ile Pro Ile Glu Ile
485 490 495

Gly Leu Leu Gln Asn Leu Gln His Leu His Ile Thr Gly Asn Lys Val
500 505 510

Asp Ile Leu Pro Lys Gln Leu Phe Lys Cys Ile Lys Leu Arg Thr Leu
515 520 525

Asn Leu Gly Gln Asn Cys Ile Thr Ser Leu Pro Glu Lys Val Gly Gln
530 535 540

Leu Ser Gln Leu Thr Gln Leu Glu Leu Lys Gly Asn Cys Leu Asp Arg
545 550 555 560

Leu Pro Ala Gln Leu Gly Gln Cys Arg Met Leu Lys Lys Ser Gly Leu
565 570 575

Val Val Glu Asp His Leu Phe Asp Thr Leu Pro Leu Glu Val Lys Glu
580 585 590

Ala Leu Asn Gln Asp Ile Asn Ile Pro Phe Ala Asn Gly Ile Xaa Thr
595 600 605

Lys Ile Ile Tyr Ala Gln
610

<210> 41
<211> 2386
<212> DNA
<213> Homo sapiens

<400> 41
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cagatttagt acaggaagca tgtgaaagtg aattgaatga agttactggt acaaagattg 180
cttatgaaac aaaaatggac ttggttcaaa catcagaagt tatgcaagag tcactctatc 240
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<210> 42
<211> 642
<212> PRT
<213> Homo sapiens

<400> 42
Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu Ala Cys Glu Ser
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Glu Leu Asn Glu Val Thr Gly Thr Lys Ile Ala Tyr Glu Thr Lys Met
20 25 30

Asp Leu Val Gln Thr Ser Glu Val Met Gln Glu Ser Leu Tyr Pro Ala
35 40 45

Ala Gln Leu Cys Pro Ser Phe Glu Glu Ser Glu Ala Thr Pro Ser Pro
50 55 60

Val Leu Pro Asp Ile Val Met Glu Ala Pro Leu Asn Ser Ala Val Pro
65 70 75 80

Ser Ala Gly Ala Ser Val Ile Gln Pro Ser Ser Ser Pro Leu Glu Ala
85 90 95

Ser Ser Val Asn Tyr Glu Ser Ile Lys His Glu Pro Glu Asn Pro Pro
100 105 110

Pro Tyr Glu Glu Ala Met Ser Val Ser Leu Lys Lys Val Ser Gly Ile
115 120 125

Lys Glu Glu Ile Lys Glu Pro Glu Asn Ile Asn Ala Ala Leu Gln Glu
130 135 140

Thr Glu Ala Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr
145 150 155 160

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Lys Leu Ser Ala Glu Pro Ala Pro Asp Phe Ser Asp Tyr Ser Glu Met
                165                 170                 175

Ala Lys Val Glu Gln Pro Val Pro Asp His Ser Glu Leu Val Glu Asp
            180                 185                 190

Ser Ser Pro Asp Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser Ile
        195                 200                 205

Pro Asp Val Pro Gln Lys Gln Asp Glu Thr Val Met Leu Val Lys Glu
    210                 215                 220

Ser Leu Thr Glu Thr Ser Phe Glu Ser Met Ile Glu Tyr Glu Asn Lys
225                 230                 235                 240

Glu Lys Leu Ser Ala Leu Pro Pro Glu Gly Gly Lys Pro Tyr Leu Glu
                245                 250                 255

Ser Phe Lys Leu Ser Leu Asp Asn Thr Lys Asp Thr Leu Leu Pro Asp
            260                 265                 270

Glu Val Ser Thr Leu Ser Lys Lys Glu Lys Ile Pro Leu Gln Met Glu
        275                 280                 285

Glu Leu Ser Thr Ala Val Tyr Ser Asn Asp Asp Leu Phe Ile Ser Lys
    290                 295                 300

Glu Ala Gln Ile Arg Glu Thr Glu Thr Phe Ser Asp Ser Ser Pro Ile
305                 310                 315                 320

Glu Ile Ile Asp Glu Phe Pro Thr Leu Ile Ser Ser Lys Thr Asp Ser
                325                 330                 335

Phe Ser Lys Leu Ala Arg Glu Tyr Thr Asp Leu Glu Val Ser His Lys
            340                 345                 350

Ser Glu Ile Ala Asn Ala Pro Asp Gly Ala Gly Ser Leu Pro Cys Thr
        355                 360                 365

Glu Leu Pro His Asp Leu Ser Leu Lys Asn Ile Gln Pro Lys Val Glu
    370                 375                 380

Glu Lys Ile Ser Phe Ser Asp Asp Phe Ser Lys Asn Gly Ser Ala Thr
385                 390                 395                 400

Ser Lys Val Leu Leu Leu Pro Pro Asp Val Ser Ala Leu Ala Thr Gln
                405                 410                 415

Ala Glu Ile Glu Ser Ile Val Lys Pro Lys Val Leu Val Lys Glu Ala
            420                 425                 430

Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp Arg Ser Pro Ser
        435                 440                 445

Ala Ile Phe Ser Ala Glu Leu Ser Lys Thr Ser Val Val Asp Leu Leu
    450                 455                 460

Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly Ala Ser Leu
465                 470                 475                 480
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Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser Val Thr Ala
485 490 495

Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser Phe Arg Ile Tyr
500 505 510

Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly His Pro Phe
515 520 525

Arg Glu Val Ala Ile Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser
530 535 540

Ala Leu Gly His Val Asn Cys Thr Ile Lys Glu Leu Arg Arg Leu Phe
545 550 555 560

Leu Val Asp Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp
565 570 575

Val Phe Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile
580 585 590

Leu Ala Leu Ile Ser Leu Phe Ser Val Pro Val Ile Tyr Glu Arg His
595 600 605

Gln Ala Gln Ile Asp His Tyr Leu Gly Leu Ala Asn Lys Asn Val Lys
610 615 620

Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu Lys Arg Lys
625 630 635 640

Ala Glu

<210> 43
<211> 344
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (13)

<220>
<221> unsure
<222> (39)

<220>
<221> unsure
<222> (185)

<220>
<221> unsure
<222> (260)

<400> 43
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gccacacggg gcgggctaca agctgctcat ccagaagttc ctcagcctgt acggcgacca 180
gatcnacatg caccgcaaat tcgtggtgca gctgttcgcc gaggagtggg gccagtacgt 240

ggacttgccc aagggcttcn cggtgagcga gcgctgcaag gtgcgcctcg tgccgctgca 300
tatccagctc actaccctgg gaaatcttac accttcaagc actg 344

<210> 44
<211> 631
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (73)

<220>
<221> unsure
<222> (369)

<400> 44
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atcattgttg gtacgtcatt ttctttaaag tgaacaattt aagaaaactt cacaagagtc 180
tgcactttgg aaagatacga tcagagtaca cagtagagac aaaacaggca tcttcattgt 240
aatttttttt aataaataaa agcacattaa caaaaaagga aggtaagcag caccggaagc 300
ctttgacgtt tgtaactaaa tgctggtact caattgaatc gagctggtta agtttcacta 360
ggaggcgcna aaaaggagcc gtttttgact taacatttta attctagtag agataagaag 420
agcttgtgtg ggcttacagt ccttcacctg actgtccttc accagtgagt agcataccag 480
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cctcactcgt ggtcactatg atcccggttc g 631

<210> 45
<211> 22
<212> PRT
<213> Homo sapiens

<400> 45
Met Val Leu Ile Ser Tyr Gln Leu Lys Gln Asn Ser Leu Thr Arg Gly
1 5 10 15

His Tyr Asp Pro Gly Ser
20

<210> 46
<211> 70
<212> DNA
<213> Homo sapiens

<400> 46
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 60
aaaaaaaaaa 70

<210> 47
<211> 428
<212> DNA
<213> Homo sapiens

<400> 47
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tcaacatgcg ctacctgggc aaggtgctgg agctggtgct gcggarcccg gcccgccacc 120
agctggacca cgtctttaaa atcggcattg gagaactcat cacccgctcg sccaagcaca 180

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tggtctccaa gaagcggaat aagaggagga aaaaccggcc cccgggggct gcagataaca 360
cagcctgggc tgtcatgacc ccccaggagc tctggaagaa catctgccag gaggccaaga 420
actacttt                                                          428

<210> 48
<211> 128
<212> PRT
<213> Homo sapiens

<220>
<221> UNSURE
<222> (21)

<220>
<221> UNSURE
<222> (43)

<400> 48
Met Arg Gln Arg Gly Ile Asn Met Arg Tyr Leu Gly Lys Val Leu Glu
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Leu Val Leu Arg Xaa Pro Ala Arg His Gln Leu Asp His Val Phe Lys
             20                  25                  30

Ile Gly Ile Gly Glu Leu Ile Thr Arg Ser Xaa Lys His Ile Phe Lys
         35                  40                  45

Thr Tyr Leu Gln Gly Val Glu Leu Ser Gly Leu Ser Ala Ala Ile Ser
     50                  55                  60

His Phe Leu Asn Cys Phe Leu Ser Ser Tyr Pro Asn Pro Val Ala His
 65                  70                  75                  80

Leu Pro Ala Asp Glu Leu Val Ser Lys Lys Arg Asn Lys Arg Arg Lys
                 85                  90                  95

Asn Arg Pro Pro Gly Ala Ala Asp Asn Thr Ala Trp Ala Val Met Thr
            100                 105                 110

Pro Gln Glu Leu Trp Lys Asn Ile Cys Gln Glu Ala Lys Asn Tyr Phe
        115                 120                 125


<210> 49
<211> 245
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (46)

<220>
<221> unsure
<222> (138)

<220>
<221> unsure
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<222> (147)

<400> 49
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cggagagccg cttatgggtg tggtccgtcc agacaccttg tttcaagggg gatgggcgtg 120
agcgggcaag cagagcancc ccaccgntga gcaagaactt tttttgtttt ttaaaccatc 180
acgtcctcat ttcacattgg aataaagtga gtttttgaaa aaaaaaaaaa aaaaaaaaaa 240
aaaaa 245

<210> 50
<211> 566
<212> DNA
<213> Homo sapiens

<400> 50
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aggtaaaaag actcaggttt gacaaagaag gtgaagtcag agaaacagcc agtcaaacga 120
cttccagcga aatttcttca gttatggtag gagaaacaga agcatcatct tcatctcagg 180
ataaagacaa agatagccgt tgtwcccggc agcactgtwc agaagaggat gaagaagagg 240
atgaagagga agaagaagag tcttttatga catcaagaga aatgatccca gaaagaaaaa 300
atcaagaaaa agaatctgat gatgccttaa ctgtgaatga agagacttct gaggaaaata 360
atcaaatgga ggaatctgat gtgtctcaag ctgagaaaga tttgctacat tctgaaggta 420
gtgaaaacga aggccctgta agtagtagtt cttctgactg ccgtgaaaca gaagaattag 480
taggatccaa ttccagtaaa actggagaga ttctttcaga atcatccatg gaaaatgatg 540
acgaagccac agaagtcacc gatgaa 566

<210> 51
<211> 141
<212> PRT
<213> Homo sapiens

<220>
<221> UNSURE
<222> (21)

<220>
<221> UNSURE
<222> (26)

<400> 51
Met Val Gly Glu Thr Glu Ala Ser Ser Ser Ser Gln Asp Lys Asp Lys
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Asp Ser Arg Cys Xaa Arg Gln His Cys Xaa Glu Glu Asp Glu Glu Glu
20 25 30

Asp Glu Glu Glu Glu Glu Glu Ser Phe Met Thr Ser Arg Glu Met Ile
35 40 45

Pro Glu Arg Lys Asn Gln Glu Lys Glu Ser Asp Asp Ala Leu Thr Val
50 55 60

Asn Glu Glu Thr Ser Glu Glu Asn Asn Gln Met Glu Glu Ser Asp Val
65 70 75 80

Ser Gln Ala Glu Lys Asp Leu Leu His Ser Glu Gly Ser Glu Asn Glu
85 90 95

Gly Pro Val Ser Ser Ser Ser Ser Asp Cys Arg Glu Thr Glu Glu Leu
100 105 110

Val Gly Ser Asn Ser Ser Lys Thr Gly Glu Ile Leu Ser Glu Ser Ser
115 120 125

Met Glu Asn Asp Asp Glu Ala Thr Glu Val Thr Asp Glu
130 135 140

<210> 52
<211> 531
<212> DNA
<213> Homo sapiens

<400> 52
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tactgactga cttgactgtc aggttcacaa cagctagatg atatatttat gactatgtct 120
aatagttgaa ataaaatctg aatattgatt tactataccc aagaggggag aaaaattaac 180
cattgtaaat ttttaaaaat tttttcaaaa atgttaaaat gaggcaaatt taagtttaca 240
aattttgaaa ttttcttttg aatatttatg aaattgtcag taaacttacc taagatcctg 300
tgaccttttg atattttttta ttttaattgt agtgccatgg accatttgta aacaaattga 360
tttacttttg ttggttgtaa gttgaagatt tagcattatg actttgaggt ctgtggtttt 420
atttgtaaac ttgcaattgc tatatttgca agggcaaatg tatttcttta ttaaataaag 480
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<210> 53
<211> 1163
<212> DNA
<213> Homo sapiens

<400> 53
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accgtcttca gcttccagac caagttcgac ttcacctcct gccagggcgt gctcttcgtg 780
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<210> 54
<211> 270
<212> PRT
<213> Homo sapiens

<400> 54
Met Lys Ala Gly Ala Phe Pro Pro Ala Pro Thr Ala Val Pro Leu His
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Pro Ser Trp Ala Tyr Val Asp Pro Ser Ser Ser Ser Ser Tyr Asp Asn
20 25 30

Gly Phe Pro Thr Gly Asp His Glu Leu Phe Thr Thr Phe Ser Trp Asp
35 40 45

Asp Gln Lys Val Arg Arg Val Phe Val Arg Lys Val Tyr Thr Ile Leu
50 55 60

Leu Ile Gln Leu Leu Val Thr Leu Ala Val Val Ala Leu Phe Thr Phe
65 70 75 80

Cys Asp Pro Val Lys Asp Tyr Val Gln Ala Asn Pro Gly Trp Tyr Trp
85 90 95

Ala Ser Tyr Ala Val Phe Phe Ala Thr Tyr Leu Thr Leu Ala Cys Cys
100 105 110

Ser Gly Pro Arg Arg His Phe Pro Trp Asn Leu Ile Leu Leu Thr Val
115 120 125

Phe Thr Leu Ser Met Ala Tyr Leu Thr Gly Met Leu Ser Ser Tyr Tyr
130 135 140

Asn Thr Thr Ser Val Leu Leu Cys Leu Gly Ile Thr Ala Leu Val Cys
145 150 155 160

Leu Ser Val Thr Val Phe Ser Phe Gln Thr Lys Phe Asp Phe Thr Ser
165 170 175

Cys Gln Gly Val Leu Phe Val Leu Leu Met Thr Leu Phe Phe Ser Gly
180 185 190

Leu Ile Leu Ala Ile Leu Leu Pro Phe Gln Tyr Val Pro Trp Leu His
195 200 205

Ala Val Tyr Ala Ala Leu Gly Ala Gly Val Phe Thr Leu Phe Leu Ala
210 215 220

Leu Asp Thr Gln Leu Leu Met Gly Asn Arg Arg His Ser Leu Ser Pro
225 230 235 240

Glu Glu Tyr Ile Phe Gly Ala Leu Asn Ile Tyr Leu Asp Ile Ile Tyr
245 250 255

Ile Phe Thr Phe Phe Leu Gln Leu Phe Gly Thr Asn Arg Glu
260 265 270

<210> 55
<211> 624
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (123)

<400> 55
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canccgggag ggcgacgtgg agcggccack tggakcggcc cgggggargc tggcggcggg 180
akgcgaggcg cgggcggcgc akcakccakg agcgcccacg gagstggacc cccagakccg 240
cgcggcgccg cagcagttcc aggaaggatg ttacctttga cgatgacagt gttaatcctg 300
ctgctgctcc ccacgggtca ggctgcccca aaggatggag tcacaaggcc agaatctgaa 360
gtgcagcatc agctcctgcc caacccctte cagccaggcc aggagcagct cggacttctg 420
cagagctacc taaagggact aggaaggaca gaagtgcaac tggagcatct gagccgggag 480
caggttctcc tctacctctt tgccctccat gactatgacc agagtggaca gctggatggc 540
ctggagctgc tgtccatgtt gacagctgct ctggcccctg gagctgccaa ctctcctacc 600
accaacccgg tgatcttgat agtg 624

<210> 56
<211> 119
<212> PRT
<213> Homo sapiens

<400> 56
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1 5 10 15

Gly Gln Ala Ala Pro Lys Asp Gly Val Thr Arg Pro Glu Ser Glu Val
20 25 30

Gln His Gln Leu Leu Pro Asn Pro Phe Gln Pro Gly Gln Glu Gln Leu
35 40 45

Gly Leu Leu Gln Ser Tyr Leu Lys Gly Leu Gly Arg Thr Glu Val Gln
50 55 60

Leu Glu His Leu Ser Arg Glu Gln Val Leu Leu Tyr Leu Phe Ala Leu
65 70 75 80

His Asp Tyr Asp Gln Ser Gly Gln Leu Asp Gly Leu Glu Leu Leu Ser
85 90 95

Met Leu Thr Ala Ala Leu Ala Pro Gly Ala Ala Asn Ser Pro Thr Thr
100 105 110

Asn Pro Val Ile Leu Ile Val
115

<210> 57
<211> 80
<212> DNA
<213> Homo sapiens

<400> 57
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aaaaaaaaaa aaaaaaaaaa 80

<210> 58
<211> 2160
<212> DNA
<213> Homo sapiens

<400> 58
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caaattaact gatcagacca caacttttca atgtttaaaa cagaataagc ttccctgtaa 180

aagcagcacc tttgtgacgt tttaacttta gtattcctct ccttcttcct caccctctcc 240
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attcctactg caagcgggag gcggaggagc gggaagcggc ggagcgcgag gcgcgcgaga 360
aagggcactt ggaacccacc gagctgctga tgaaccgggc ttacttgcag agcattaccc 420
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cgatacgaga tgaagaagag actggagatc actccatgga cgatagttcg gaggatggga 660
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<210> 59
<211> 141
<212> PRT
<213> Homo sapiens

<400> 59
Met Asn His Arg Tyr Ser Tyr Cys Lys Arg Glu Ala Glu Glu Arg Glu
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Ala Ala Glu Arg Glu Ala Arg Glu Lys Gly His Leu Glu Pro Thr Glu
20 25 30

Leu Leu Met Asn Arg Ala Tyr Leu Gln Ser Ile Thr Pro Gln Gly Tyr
35 40 45

Ser Asp Ser Glu Glu Arg Glu Ser Met Pro Arg Asp Gly Glu Ser Glu
50 55 60

Lys Glu His Glu Lys Glu Gly Glu Asp Gly Tyr Gly Lys Leu Gly Arg
65 70 75 80

Gln Asp Gly Asp Glu Glu Phe Glu Glu Glu Glu Glu Glu Ser Glu Asn
85 90 95

Lys Ser Met Asp Thr Asp Pro Glu Thr Ile Arg Asp Glu Glu Glu Thr
100 105 110

Gly Asp His Ser Met Asp Asp Ser Ser Glu Asp Gly Lys Met Glu Thr
115 120 125

Lys Ser Asp His Glu Glu Asp Asn Met Glu Asp Gly Met
130 135 140

<210> 60
<211> 2168
<212> DNA
<213> Homo sapiens

<400> 60
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agtatgagac gaacaaagtc actcggatcc agagcatgaa ttatggcacc attaagtggt 180
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aagaggagat cgtggagaat ggagtgaaga agttggtgca cagtgtcttt gacaccgcag 360
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ccttgctggc gctggatgtg gattccacca acagccggct gcggcactgt gcctacaggt 1740
gctacgccac ctggcgcttc ggctcccagg acatggctga ctttgccatc ctgcccagct 1800
gctgccgctg gaggatccgg aaagagtttc cgaagagtga agggcagtac agtggcttca 1860
agagtcctta ctgaagccag gcgccgtggc tcacgtctgt aatcccagcg ctttgggagg 1920
ccgaggcagg cagatcacct gaggtcggga gttggagacc cgcctggcta acaaggcgaa 1980
atcctgtctg tactaaaaat acaaaaatca gccagacatg gtggcatgca cctgcaatcc 2040
cagctactcg ggaggctgag gcacaagaat cacttgaacc cgggaggcag aggttgtagt 2100
gagcccagat tgtgccactg ctctccagcc tgggaggcac agcaaactgt ccccaaaaaa 2160
aaaaaaaa 2168

<210> 61
<211> 595
<212> PRT
<213> Homo sapiens

<400> 61
Met Pro Ala Cys Cys Ser Cys Ser Asp Val Phe Gln Tyr Glu Thr Asn
1 5 10 15

Lys Val Thr Arg Ile Gln Ser Met Asn Tyr Gly Thr Ile Lys Trp Phe
20 25 30

Phe His Val Ile Ile Phe Ser Tyr Val Cys Phe Ala Leu Val Ser Asp
35 40 45

Lys Leu Tyr Gln Arg Lys Glu Pro Val Ile Ser Ser Val His Thr Lys
50 55 60

Val Lys Gly Ile Ala Glu Val Lys Glu Glu Ile Val Glu Asn Gly Val
65 70 75 80

Lys Lys Leu Val His Ser Val Phe Asp Thr Ala Asp Tyr Thr Phe Pro
85 90 95

Leu Gln Gly Asn Ser Phe Phe Val Met Thr Asn Phe Leu Lys Thr Glu
100 105 110

Gly Gln Glu Gln Arg Leu Cys Pro Glu Tyr Pro Thr Arg Arg Thr Leu
115 120 125

Cys Ser Ser Asp Arg Gly Cys Lys Lys Gly Trp Met Asp Pro Gln Ser
130 135 140

Lys Gly Ile Gln Thr Gly Arg Cys Val Val His Glu Gly Asn Gln Lys
145 150 155 160

Thr Cys Glu Val Ser Ala Trp Cys Pro Ile Glu Ala Val Glu Glu Ala
165 170 175

Pro Arg Pro Ala Leu Leu Asn Ser Ala Glu Asn Phe Thr Val Leu Ile
180 185 190

Lys Asn Asn Ile Asp Phe Pro Gly His Asn Tyr Thr Thr Arg Asn Ile
195 200 205

Leu Pro Gly Leu Asn Ile Thr Cys Thr Phe His Lys Thr Gln Asn Pro
210 215 220

Gln Cys Pro Ile Phe Arg Leu Gly Asp Ile Phe Arg Glu Thr Gly Asp
225 230 235 240

Asn Phe Ser Asp Val Ala Ile Gln Gly Gly Ile Met Gly Ile Glu Ile
245 250 255

Tyr Trp Asp Cys Asn Leu Asp Arg Trp Phe His His Cys His Pro Lys
260 265 270

Tyr Ser Phe Arg Arg Leu Asp Asp Lys Thr Thr Asn Val Ser Leu Tyr
275 280 285

Pro Gly Tyr Asn Phe Arg Tyr Ala Lys Tyr Tyr Lys Glu Asn Asn Val
290 295 300

Glu Lys Arg Thr Leu Ile Lys Val Phe Gly Ile Arg Phe Asp Ile Leu
305 310 315 320

Val Phe Gly Thr Gly Gly Lys Phe Asp Ile Ile Gln Leu Val Val Tyr
325 330 335

Ile Gly Ser Thr Leu Ser Tyr Phe Gly Leu Ala Ala Val Phe Ile Asp
340 345 350

Phe Leu Ile Asp Thr Tyr Ser Ser Asn Cys Cys Arg Ser His Ile Tyr
355 360 365

Pro Trp Cys Lys Cys Cys Gln Pro Cys Val Val Asn Glu Tyr Tyr Tyr
370 375 380

Arg Lys Lys Cys Glu Ser Ile Val Glu Pro Lys Pro Thr Leu Lys Tyr
385 390 395 400

Val Ser Phe Val Asp Glu Ser His Ile Arg Met Val Asn Gln Gln Leu
405 410 415

Leu Gly Arg Ser Leu Gln Asp Val Lys Gly Gln Glu Val Pro Arg Pro
420 425 430

Ala Met Asp Phe Thr Asp Leu Ser Arg Leu Pro Leu Ala Leu His Asp
435 440 445

Thr Pro Pro Ile Pro Gly Gln Pro Glu Glu Ile Gln Leu Leu Arg Lys
450 455 460

Glu Ala Thr Pro Arg Ser Arg Asp Ser Pro Val Trp Cys Gln Cys Gly
465 470 475 480

Ser Cys Leu Pro Ser Gln Leu Pro Glu Ser His Arg Cys Leu Glu Glu
485 490 495

Leu Cys Cys Arg Lys Lys Pro Gly Ala Cys Ile Thr Thr Ser Glu Leu
500 505 510

Phe Arg Lys Leu Val Leu Ser Arg His Val Leu Gln Phe Leu Leu Leu
515 520 525

Tyr Gln Glu Pro Leu Leu Ala Leu Asp Val Asp Ser Thr Asn Ser Arg
530 535 540

Leu Arg His Cys Ala Tyr Arg Cys Tyr Ala Thr Trp Arg Phe Gly Ser
545 550 555 560

Gln Asp Met Ala Asp Phe Ala Ile Leu Pro Ser Cys Cys Arg Trp Arg
565 570 575

Ile Arg Lys Glu Phe Pro Lys Ser Glu Gly Gln Tyr Ser Gly Phe Lys
580 585 590

Ser Pro Tyr
595

<210> 62
<211> 430
<212> DNA
<213> Homo sapiens

<400> 62
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ctcaggtaat tggtatgtga aaaagtgtct aaacgacgtt ggaatttgca agaagaagtg 180
caaacctgaa gagatgcatg taaagaatgg ttgggcaatg tgcggcaaac aaagggactg 240
ctgtgttcca gctgacagac gtgctaatta tcctgttttc tgtgtccaga caaagactac 300
aagaatttca acagtaacag caacaacagc aacaacaact ttgatgatga ctactgcttc 360
gatgtcttcg atggctccta cccgtttctc ccactggttg aacattccag cctctgtctc 420
ctgctctagg                                                        430
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<210> 63
<211> 121
<212> PRT
<213> Homo sapiens

<400> 63

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Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln
  1               5                  10                  15

Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly
             20                  25                  30

Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly
         35                  40                  45

Trp Ala Met Cys Gly Lys Gln Arg Asp Cys Cys Val Pro Ala Asp Arg
     50                  55                  60

Arg Ala Asn Tyr Pro Val Phe Cys Val Gln Thr Lys Thr Thr Arg Ile
 65                  70                  75                  80

Ser Thr Val Thr Ala Thr Thr Ala Thr Thr Thr Leu Met Met Thr Thr
                 85                  90                  95

Ala Ser Met Ser Ser Met Ala Pro Thr Arg Phe Ser His Trp Leu Asn
            100                 105                 110

Ile Pro Ala Ser Val Ser Cys Ser Arg
        115                 120
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<210> 64
<211> 112
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (8)

<220>
<221> unsure
<222> (12)

<220>
<221> unsure
<222> (36)

<220>
<221> unsure
<222> (41)

<220>
<221> unsure
<222> (44)

<400> 64
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 112

<210> 65
<211> 324
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (1)

<220>
<221> unsure
<222> (69)

<220>
<221> unsure
<222> (74)

<220>
<221> unsure
<222> (125)

<220>
<221> unsure
<222> (159)

<400> 65
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gggtgtacnc gtangggtct gtgtgctggg ggtggctcac cgggcagcgt gggtgagcgg 120
cgcancggcg gcagcggaga acgagagagg ggagcagana cagaatcgcc taagctgaag 180
tgtattggcg ccatcatggc tcactgcggc ctccggctcc ttggctcggg tgattctcct 240
gcctgagcct ccctagtagc taggactaca gtgctgtaga agaaaatcac atgattggtg 300
ccctcaaaaa attggtgcca cttg 324

<210> 66
<211> 794
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (61)

<220>
<221> unsure
<222> (82)

<220>
<221> unsure
<222> (108)..(120)

<220>
<221> unsure

<222> (184)

<220>
<221> unsure
<222> (754)

<400> 66
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naaagcacag attcagcaat cnacacacac tcatctggat atctcacnnn nnnnnnnnnn 120
ttaactgatg aaaaaagtaa tggaacaatt gcccttgtgg atgattctga ggatcctgga 180
gccnatgtat ctaacataca gcttcagcaa aaaatttcaa gtctggagat taaactcaaa 240
gtatctgaag aagaaaaaca gagaattaaa caggatgtgg aakcattgat ggaaaagcat 300
aatgtcttag aaaaaggctt tctaaaagaa aaagagcaag aggccatttc ttttcaagat 360
agatacaaag aacttcagga aaaacataaa caagaattgg aagacatgag gaaagctggt 420
cacgaagccc tcagcattat tgtggatgaa tataaggcac tactgcagtc ttcagttaag 480
caacaagtag aagctattga aaaacagtac atttctgcaa ttgagaaaca ggcacacaag 540
tgtgaggagt tgctaaatgc tcagcatcag aggctccttg aagtgctaga tacagagaag 600
gaactgttaa aagaaaaaat aaaggaagct ttgattcagc aatctcaaga acagaaggaa 660
atattggaaa agtgtttgga ggaagaaagg caaagaaata aagaggcatt agtatccgct 720
gcaaagcttg aaaaagaacc agtgaaggat gcantttaa aattcgtaga agaagaaaga 780
aaaaaaaaaa aaaa 794

<210> 67
<211> 164
<212> PRT
<213> Homo sapiens

<220>
<221> UNSURE
<222> (156)

<400> 67
Met Glu Lys His Asn Val Leu Glu Lys Gly Phe Leu Lys Glu Lys Glu
1 5 10 15

Gln Glu Ala Ile Ser Phe Gln Asp Arg Tyr Lys Glu Leu Gln Glu Lys
20 25 30

His Lys Gln Glu Leu Glu Asp Met Arg Lys Ala Gly His Glu Ala Leu
35 40 45

Ser Ile Ile Val Asp Glu Tyr Lys Ala Leu Leu Gln Ser Ser Val Lys
50 55 60

Gln Gln Val Glu Ala Ile Glu Lys Gln Tyr Ile Ser Ala Ile Glu Lys
65 70 75 80

Gln Ala His Lys Cys Glu Glu Leu Leu Asn Ala Gln His Gln Arg Leu
85 90 95

Leu Glu Val Leu Asp Thr Glu Lys Glu Leu Leu Lys Glu Lys Ile Lys
100 105 110

Glu Ala Leu Ile Gln Gln Ser Gln Glu Gln Lys Glu Ile Leu Glu Lys
115 120 125

Cys Leu Glu Glu Glu Arg Gln Arg Asn Lys Glu Ala Leu Val Ser Ala
130 135 140

Ala Lys Leu Glu Lys Glu Pro Val Lys Asp Ala Xaa Leu Lys Phe Val

145 150 155 160

Glu Glu Glu Arg

<210> 68
<211> 1494
<212> DNA
<213> Homo sapiens

<400> 68
cgtttgtcga cgccgctgcc accgcctgcc tgagagaagt cgtcgcggcc gaccccgtcg 60
cctccgccgg ctaccatgtc cgcccaggcg cagatgcggg ccctgctgga ccagctcatg 120
ggcacggctc gggacggaga cgaaaccaga cagagggtca agtttacaga tgaccgtgtc 180
tgcaagagtc accttctgga ctgctgcccc catgacatcc tggctgggac gcgcatggat 240
ttaggagaat gtaccaaaat ccacgacttg gccctccgag cagattatga gattgcaagt 300
aaagaaagag acctgttttt tgaattagat gcaatggatc acttggagtc ctttattgct 360
gaatgtgatc ggagaactga gctcgccaag aagcggctgg cagaaacaca ggaggaaatc 420
agtgcggaag tttctgcaaa ggcaggaaaa gtacatgagt taaatgaaga aataggaaaa 480
ctccttgcta aagccgaaca gctaggggct gaaggtaatg tggatgaatc ccagaagatt 540
cttatggaag tggaaaaagt tcgtgcgaag aaaaaagaag ctgaggaaga atacagaaat 600
tccatgcctg catccagttt tcagcagcaa aagctgcgtg tctgcgaggt ctgttcagcc 660
taccttggtc tccatgacaa tgaccgtcgc ctggcagacc acttcggtgg caagttacac 720
ttggggttca ttcagatccg agagaagctt gatcagttga ggaaaactgt cgctgaaaag 780
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gcttcccggg accgaagtgc gaaatacaag taactactct gactccttcg gtagctgcaa 1080
ccaggagttc tccagagagc gggcatccag agaggagtcc tgggagagcg ggcggagcga 1140
gcgagggccc ccggactgga ggcttgagag ctccaacggg aagatggctt cacggaggtc 1200
agaagagaag gaggccggcg agatctgaac ccgtctcccg ggtgctgtaa atagtctgat 1260
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gtttaaaatt tctattgttt tggagctagc tgtgagtttc tagaagtgta cagagttgct 1380
cctgtgttcc cgggtcatgt tgagtaggaa taaataaatc tgatgctgcc tcctggaaaa 1440
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1494

<210> 69
<211> 325
<212> PRT
<213> Homo sapiens

<400> 69
Met Ser Ala Gln Ala Gln Met Arg Ala Leu Leu Asp Gln Leu Met Gly
1 5 10 15

Thr Ala Arg Asp Gly Asp Glu Thr Arg Gln Arg Val Lys Phe Thr Asp
20 25 30

Asp Arg Val Cys Lys Ser His Leu Leu Asp Cys Cys Pro His Asp Ile
35 40 45

Leu Ala Gly Thr Arg Met Asp Leu Gly Glu Cys Thr Lys Ile His Asp
50 55 60

Leu Ala Leu Arg Ala Asp Tyr Glu Ile Ala Ser Lys Glu Arg Asp Leu
65 70 75 80

Phe Phe Glu Leu Asp Ala Met Asp His Leu Glu Ser Phe Ile Ala Glu

85 90 95

Cys Asp Arg Arg Thr Glu Leu Ala Lys Lys Arg Leu Ala Glu Thr Gln
100 105 110

Glu Glu Ile Ser Ala Glu Val Ser Ala Lys Ala Gly Lys Val His Glu
115 120 125

Leu Asn Glu Glu Ile Gly Lys Leu Leu Ala Lys Ala Glu Gln Leu Gly
130 135 140

Ala Glu Gly Asn Val Asp Glu Ser Gln Lys Ile Leu Met Glu Val Glu
145 150 155 160

Lys Val Arg Ala Lys Lys Lys Glu Ala Glu Glu Glu Tyr Arg Asn Ser
165 170 175

Met Pro Ala Ser Ser Phe Gln Gln Gln Lys Leu Arg Val Cys Glu Val
180 185 190

Cys Ser Ala Tyr Leu Gly Leu His Asp Asn Asp Arg Arg Leu Ala Asp
195 200 205

His Phe Gly Gly Lys Leu His Leu Gly Phe Ile Gln Ile Arg Glu Lys
210 215 220

Leu Asp Gln Leu Arg Lys Thr Val Ala Glu Lys Gln Glu Lys Arg Asn
225 230 235 240

Gln Asp Arg Leu Arg Arg Arg Glu Glu Arg Glu Arg Glu Glu Arg Leu
245 250 255

Ser Arg Arg Ser Gly Ser Arg Thr Arg Asp Arg Arg Arg Ser Arg Ser
260 265 270

Arg Asp Arg Arg Arg Arg Arg Ser Arg Ser Thr Ser Arg Glu Arg Arg
275 280 285

Lys Leu Ser Arg Ser Arg Ser Arg Asp Arg His Arg Arg His Arg Ser
290 295 300

Arg Ser Arg Ser His Ser Arg Gly His Arg Arg Ala Ser Arg Asp Arg
305 310 315 320

Ser Ala Lys Tyr Lys
325

<210> 70
<211> 1761
<212> DNA
<213> Homo sapiens

<400> 70
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acccctgcat ggcagaaact gtgcagggga cgaggccaag gaatcaggag acccagaggc 120
aggggtggcc cggagacggt gaagaaacca agacgcagag aggccaagcc ccttgccttg 180
ggtcacacag ccaaaggagg cagagccaga actcacaacc agatccagag gcaacaggga 240
catggccacc tgggacgaaa aggcagtcac ccgcagggcc aaggtggctc ccgctgagag 300
gatgagcaag ttcttaaggc acttcacggt cgtgggagac gactaccatg cctggaacat 360

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caactacaag aaatgggaga atgaagagga ggaggaggag gaggagcagc caccacccac 420
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cgcacccagg gcccccttg acttcagggg catgttgagg aaactgttca gctcccacag 540
gtttcaggtc atcatcatct gcttggtggt tctggatgcc ctcctggtgc ttgctgagct 600
catcctggac ctgaagatca tccagcccga caagaataac tatgctgcca tggtattcca 660
ctacatgagc atcaccatct tggtcttttt tatgatggag atcatcttta aattatttgt 720
cttccgcctg gagttctttc accacaagtt tgagatcctg gatgccgtcg tggtggtggt 780
ctcattcatc ctcgacattg tcctcctgtt ccaggagcac cagtttgagg ctctgggcct 840
gctgattctg ctccggctgt ggcgggtggc ccggatcatc aatgggatta tcatctcagt 900
taagacacgt tcagaacggc aactcttaag gttaaaacag atgaatgtac aattggccgc 960
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aatgagcaac aaagctggac aattgctagt tgtatataaa atttaatctc accgaatgta 1380
cagttttcaa atttcacgtg tatattaagg aactgatgca tctgagcatt ctgaaagaaa 1440
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ccagctgcat cagccagctt ctaggtggct ccattgtttt ctgccacctg acaacatttt 1620
tcctcaatta ctgtacaact actgtataaa ataaaacaac tactgtataa aataaactct 1680
ctcttttccc tggaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1740
aaaaaaaaaa aaaaaaaaaa a                                           1761

&lt;210&gt; 71
&lt;211&gt; 273
&lt;212&gt; PRT
&lt;213&gt; Homo sapiens

&lt;400&gt; 71
Met Ala Thr Trp Asp Glu Lys Ala Val Thr Arg Arg Ala Lys Val Ala
1               5                   10                  15

Pro Ala Glu Arg Met Ser Lys Phe Leu Arg His Phe Thr Val Val Gly
            20                  25                  30

Asp Asp Tyr His Ala Trp Asn Ile Asn Tyr Lys Lys Trp Glu Asn Glu
        35                  40                  45

Glu Glu Glu Glu Glu Glu Glu Gln Pro Pro Pro Thr Pro Val Ser Gly
    50                  55                  60

Glu Glu Gly Arg Ala Ala Ala Pro Asp Val Ala Pro Ala Pro Gly Pro
65                  70                  75                  80

Ala Pro Arg Ala Pro Leu Asp Phe Arg Gly Met Leu Arg Lys Leu Phe
                85                  90                  95

Ser Ser His Arg Phe Gln Val Ile Ile Ile Cys Leu Val Val Leu Asp
            100                 105                 110

Ala Leu Leu Val Leu Ala Glu Leu Ile Leu Asp Leu Lys Ile Ile Gln
        115                 120                 125

Pro Asp Lys Asn Asn Tyr Ala Ala Met Val Phe His Tyr Met Ser Ile
    130                 135                 140

Thr Ile Leu Val Phe Phe Met Met Glu Ile Ile Phe Lys Leu Phe Val
145                 150                 155                 160
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Phe Arg Leu Glu Phe Phe His His Lys Phe Glu Ile Leu Asp Ala Val
165 170 175

Val Val Val Val Ser Phe Ile Leu Asp Ile Val Leu Leu Phe Gln Glu
180 185 190

His Gln Phe Glu Ala Leu Gly Leu Leu Ile Leu Leu Arg Leu Trp Arg
195 200 205

Val Ala Arg Ile Ile Asn Gly Ile Ile Ile Ser Val Lys Thr Arg Ser
210 215 220

Glu Arg Gln Leu Leu Arg Leu Lys Gln Met Asn Val Gln Leu Ala Ala
225 230 235 240

Lys Ile Gln His Leu Glu Phe Ser Cys Ser Glu Lys Glu Gln Glu Ile
245 250 255

Glu Arg Leu Asn Lys Leu Leu Arg Gln His Gly Leu Leu Gly Glu Val
260 265 270

Asn

<210> 72
<211> 928
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (367)

<220>
<221> unsure
<222> (448)

<220>
<221> unsure
<222> (467)

<220>
<221> unsure
<222> (508)

<220>
<221> unsure
<222> (539)

<400> 72
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catgaataca acctaacgca tctgcagcct tccacagatt atgaagtgtg tctcacagtg 180
tccaatattc atcagcagac tcaaaagtca tgcgtaaatg tcacaaccaa aaatgccgcc 240
ttcgcagtgg acatctctga tcaagaaacc agtacagccc ttgctgcagt aatggggtmt 300
atgtttgccg tcattagcct tgcgtccatt gctgtggtac tttgccaaaa gatttaagag 360
aaaaaantac caccactcat taaaaaagta tatgcaaaaa acctcttcaa tcccactaaa 420
tgagctgtac ccaccactca ttaacctntg ggaaggtgac agcgagnaag acaaagatgg 480

ttttgcagac accaagccaa cccaggtnga cacatccaga aggtattaca tgtggtaant 540
cagaggatat tttgcttctg gtagtaagga gcacaaagac gtttttgctt tattctgcaa 600
aagtgaacaa gttgaagact tttgtatttt tgactttgct agtttgtggc agagtggaga 660
ggacgggtgg atatttcaaa tttttttagt atagcgtatc gcaagggttt gacacggctg 720
ccagcgactc taggcttcca gtctgtgttt ggtttttatt cttatcatta ttatgattgt 780
tattatatta ttattttatt ttagttgttg tgctaaactc aataatgctg ttctaactac 840
agtgctcaat aaaatgatta atgacaggat ggggttcccc tgtgctttta ccagtagcat 900
gacccttcct gaagccatcc gtagaaag 928

<210> 73
<211> 52
<212> PRT
<213> Homo sapiens

<400> 73
Met Ile Val Ile Ile Leu Leu Phe Tyr Phe Ser Cys Cys Ala Lys Leu
1 5 10 15

Asn Asn Ala Val Leu Thr Thr Val Leu Asn Lys Met Ile Asn Asp Arg
20 25 30

Met Gly Phe Pro Cys Ala Phe Thr Ser Ser Met Thr Leu Pro Glu Ala
35 40 45

Ile Arg Arg Lys
50

<210> 74
<211> 49
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (9)

<400> 74
aaattaaana aaaaaaaaaa aaaaaaaaaa aaataaagaa aaaaaaaaa 49

<210> 75
<211> 597
<212> DNA
<213> Homo sapiens

<400> 75
attctacaag ataacttccc agtactttaa aaaagtctca aagtcataaa caagaaagaa 60
ctgagggact attgcatatt ggagcgatct aaagaagtat tacaatttgt ggaattcttg 120
attaaatcct ggaccagcaa aaggacatta gtgggaaaat tgatgaaatt caaatgagat 180
cttatattga agttaattgt gtcagtgtac atttcctggt tttcataatt gcaagtgatt 240
atgtaaggtt tgttaatatt aggagcagct gggtaaaggt tatacaaaaa ctctatacta 300
tttttgcatt tttttctgta agtttaaaac attttccaac taaaaagttg aaaacacatg 360
tattagagac acatgcgtat gtgtctctaa taatcttaaa tatatttaag atgatagaag 420
gaattcttga gatagtaaaa tgaagtcacc aaaaaacaaa caaagaaaca aaacgaaatc 480
accaaaatct atcaataaat ttcaggtaat acttttggca gattcattcc tttgagatgg 540
agtctcactc ccagtctggg caacgagcga aactccgtct aaaaaaaaaa aaaaaaa 597

<210> 76
<211> 89
<212> PRT

<213> Homo sapiens

<400> 76
Met Arg Ser Tyr Ile Glu Val Asn Cys Val Ser Val His Phe Leu Val
1   5   10   15

Phe Ile Ile Ala Ser Asp Tyr Val Arg Phe Val Asn Ile Arg Ser Ser
            20   25   30

Trp Val Lys Val Ile Gln Lys Leu Tyr Thr Ile Phe Ala Phe Phe Ser
        35   40   45

Val Ser Leu Lys His Phe Pro Thr Lys Lys Leu Lys Thr His Val Leu
    50   55   60

Glu Thr His Ala Tyr Val Ser Leu Ile Ile Leu Asn Ile Phe Lys Met
65   70   75   80

Ile Glu Gly Ile Leu Glu Ile Val Lys
                85

<210> 77
<211> 1804
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (1794)

<400> 77
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<210> 78
<211> 37
<212> PRT
<213> Homo sapiens

<400> 78
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1 5 10 15

Thr Pro Ser Ala Ser Arg Thr Gln Lys Asn Met Leu Lys Glu Tyr Pro
20 25 30

Ile Phe Trp Ile Asn
35

<210> 79
<211> 360
<212> DNA
<213> Homo sapiens

<400> 79
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<210> 80
<211> 20
<212> PRT
<213> Homo sapiens

<400> 80
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1 5 10 15

Ser Lys Pro Val
20

<210> 81
<211> 202
<212> DNA
<213> Homo sapiens

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<222> (136)

<220>
<221> unsure
<222> (138)

<400> 81

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aaaaaaaaaa aaaaantnaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 180
aaaaaaaaaa aaaaaaaaaa aa 202

<210> 82
<211> 1189
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (1155)

<400> 82
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cagtatggta tgattaaatc aagttattaa cctatccttc acgttaaatg cttaaatttt 600
ttgatgagaa catttgaaat ttactcttgg aaggtaaaaa aaaatctcag gaccccccaa 660
attaaagcca tgaagctgaa ttgtgcaaca tcctcttcca aatggaagct tgtcttccag 720
gtacagaaca aaaacaagac tcatttcttc acctgcctaa agatgtgcac ataattggct 780
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gtcactgtct taccaatttg aaatgtaaaa tattytacta ctaattatat ttaccacatt 1140
gtgcaacaga actcnaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaa 1189

<210> 83
<211> 56
<212> PRT
<213> Homo sapiens

<400> 83
Met Arg Thr Phe Glu Ile Tyr Ser Trp Lys Val Lys Lys Asn Leu Arg
1 5 10 15

Thr Pro Gln Ile Lys Ala Met Lys Leu Asn Cys Ala Thr Ser Ser Ser
20 25 30

Lys Trp Lys Leu Val Phe Gln Val Gln Asn Lys Asn Lys Thr His Phe
35 40 45

Phe Thr Cys Leu Lys Met Cys Thr
50 55

<210> 84
<211> 525
<212> DNA
<213> Homo sapiens

<400> 84
cataacagcg tcagagagaa agaactgact gaaacgtttg agatgaagaa agttctcctc 60
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gaaaaaagaa gtatcagtga cagcgatgaa ttagcttcag ggttttttgt gttcccttac 180
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acaagaagga aaagtcacga taaacctggt cacctgaaat tgaaattgag ccacttcctt 360
gaagaatcaa aattcctgtt aataaaagaa aaacaaatgt aattgaaata gcacacagca 420
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 525

<210> 85
<211> 85
<212> PRT
<213> Homo sapiens

<400> 85
Met Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val
1 5 10 15

Gly Phe Pro Val Ser Gln Asp Gln Glu Arg Glu Lys Arg Ser Ile Ser
20 25 30

Asp Ser Asp Glu Leu Ala Ser Gly Phe Phe Val Phe Pro Tyr Pro Tyr
35 40 45

Pro Phe Arg Pro Leu Pro Pro Ile Pro Phe Pro Arg Phe Pro Trp Phe
50 55 60

Arg Arg Asn Phe Pro Ile Pro Ile Pro Glu Ser Ala Pro Thr Thr Pro
65 70 75 80

Leu Pro Ser Glu Lys
85

<210> 86
<211> 349
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (9)

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<222> (188)

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<222> (230)

<220>
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<220>
<221> unsure
<222> (270)

<400> 86
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tctttcanac aacattcttc ttaacattgc tgtccttgag gacttaccan antgaagtct 240
tggctgaacg tttaccattg actcctgttn tcacttaaag tttccaccaa ttctacgcgt 300
cagagtttgc acttacaatg gactgtccac aaccttcctt atcatcagg 349

<210> 87
<211> 563
<212> DNA
<213> Homo sapiens

<220>
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<222> (63)

<220>
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<222> (83)

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<400> 87
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ttnttttgga aaccccaacc tggagatgtt ataggttatg ttgtggantg gtgtgaccan 240
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gttggaaaga ttactctact gaatctcaac ctggttttat acaagggtac catgtctatc 540
tgaaatccaa ggcgaggcag tgc 563

<210> 88
<211> 58

<212> PRT
<213> Homo sapiens

<400> 88
Arg Lys Lys Thr Gly Tyr Ser Gln Glu Leu Ala Pro Ser Asp Asn Pro
1 5 10 15

His Val Leu Val Asp Thr Leu Thr Ser His Ser Phe Thr Leu Ser Trp
20 25 30

Lys Asp Tyr Ser Thr Glu Ser Gln Pro Gly Phe Ile Gln Gly Tyr His
35 40 45

Val Tyr Leu Lys Ser Lys Ala Arg Gln Cys
50 55

<210> 89
<211> 361
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (102)

<220>
<221> unsure
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<220>
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<400> 89
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gaacantcct ngatgctgat tcatatccta ctgcccatgg ttttctgcgt cttgctcatc 240
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gacccttaca agagcagcat cctgtcatta ataaaattca aggtaaaaaa aaaaaaaaaa 360
a 361

<210> 90
<211> 756
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (37)

<220>
<221> unsure
<222> (54)

<220>
<221> unsure
<222> (376)

<220>
<221> unsure
<222> (433)

<400> 90
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ttcagagctc cattccattc cagcaccagc caacagcaca aaactaatcc ttgacaggtg 240
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<210> 91
<211> 58
<212> PRT
<213> Homo sapiens

<400> 91
Arg Lys Lys Thr Gly Tyr Ser Gln Glu Leu Ala Pro Ser Asp Asn Pro
1 5 10 15

His Val Leu Val Asp Thr Leu Thr Ser His Ser Phe Thr Leu Ser Trp
20 25 30

Lys Asp Tyr Ser Thr Glu Ser Gln Pro Gly Phe Ile Gln Gly Tyr His
35 40 45

Val Tyr Leu Lys Ser Lys Ala Arg Gln Cys
50 55

<210> 92
<211> 79
<212> DNA
<213> Homo sapiens

<400> 92
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aaaaaaaaaa aaaaaaaaa 79

<210> 93

<211> 1939
<212> DNA
<213> Homo sapiens

<400> 93
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<210> 94
<211> 52
<212> PRT
<213> Homo sapiens

<400> 94
Met Ser Val Arg Phe Ile Val Met Phe Pro Phe Leu Phe Leu Thr Leu
1 5 10 15

Leu Ile Cys Val Leu Ser Pro Ser Ile Pro Leu Ser Leu Ser Leu Val
20 25 30

Ser Trp Ser Val Gly Leu Ser Pro Leu Leu Ile Phe Ser Glu Asn His
35 40 45

Phe Leu Phe Leu
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<210> 95
<211> 1252

<212> DNA
<213> Homo sapiens

<400> 95
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<210> 96
<211> 289
<212> PRT
<213> Homo sapiens

<400> 96
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            20                  25                  30

Ser Asn Ser Asn Ile His Pro Ile Phe Ser Trp Cys Gly Ser Thr Asp
        35                  40                  45

Ser Lys Asp Ile Val Met Pro Thr Tyr Asp Leu Thr Asp Ser Val Leu
    50                  55                  60

Glu Thr Met Gly Arg Val Ser Leu Asp Met Met Ser Val Gln Ala Asn
65                  70                  75                  80

Thr Gly Pro Pro Trp Glu Ser Lys Asn Ser Thr Ala Val Trp Arg Gly
                85                  90                  95

Arg Asp Ser Arg Lys Glu Arg Leu Glu Leu Val Lys Leu Ser Arg Lys
            100                 105                 110

His Pro Glu Leu Ile Asp Ala Ala Phe Thr Asn Phe Phe Phe Phe Lys
        115                 120                 125

His Asp Glu Asn Leu Tyr Gly Pro Ile Val Lys His Ile Ser Phe Phe
    130                 135                 140

Asp Phe Phe Lys His Lys Tyr Gln Ile Asn Ile Asp Gly Thr Val Ala
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145 150 155 160

Ala Tyr Arg Leu Pro Tyr Leu Leu Val Gly Asp Ser Val Val Leu Lys
165 170 175

Gln Asp Ser Ile Tyr Tyr Glu His Phe Tyr Asn Glu Leu Gln Pro Trp
180 185 190

Lys His Tyr Ile Pro Val Lys Ser Asn Leu Ser Asp Leu Leu Glu Lys
195 200 205

Leu Lys Trp Ala Lys Asp His Asp Glu Glu Ala Lys Lys Ile Ala Lys
210 215 220

Ala Gly Gln Glu Phe Ala Arg Asn Asn Leu Met Gly Asp Asp Ile Phe
225 230 235 240

Cys Tyr Tyr Phe Lys Leu Phe Gln Glu Tyr Ala Asn Leu Gln Val Ser
245 250 255

Glu Pro Gln Ile Arg Glu Gly Met Lys Arg Val Glu Pro Gln Thr Glu
260 265 270

Asp Asp Leu Phe Pro Cys Thr Cys His Arg Lys Lys Thr Lys Asp Glu
275 280 285

Leu

<210> 97
<211> 492
<212> DNA
<213> Homo sapiens

<400> 97
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gaagatccaa ctaacactgc tgcaagaaag cgtaagattg ccattcgaaa agcccagggg 420
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gaagcctggc at 492

<210> 98
<211> 159
<212> PRT
<213> Homo sapiens

<400> 98
Met Ala Lys Val Ser Glu Leu Tyr Asp Val Thr Trp Glu Glu Met Arg
1 5 10 15

Asp Lys Met Arg Lys Trp Arg Glu Glu Asn Ser Arg Asn Ser Glu Gln
20 25 30

Ile Val Glu Val Gly Glu Glu Leu Ile Asn Glu Tyr Ala Ser Lys Leu
35 40 45

Gly Asp Asp Ile Trp Ile Ile Tyr Glu Gln Val Met Ile Ala Ala Leu
50 55 60

Asp Tyr Gly Arg Asp Asp Leu Ala Leu Phe Cys Leu Gln Glu Leu Arg
65 70 75 80

Arg Gln Phe Pro Gly Ser His Arg Val Lys Arg Leu Thr Gly Met Arg
85 90 95

Phe Glu Ala Met Glu Arg Tyr Asp Asp Ala Ile Gln Leu Tyr Asp Arg
100 105 110

Ile Leu Gln Glu Asp Pro Thr Asn Thr Ala Ala Arg Lys Arg Lys Ile
115 120 125

Ala Ile Arg Lys Ala Gln Gly Lys Asn Val Glu Ala Ile Arg Glu Leu
130 135 140

Asn Glu Tyr Leu Glu Gln Phe Val Gly Asp Gln Glu Ala Trp His
145 150 155

<210> 99
<211> 85
<212> DNA
<213> Homo sapiens

<220>
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<222> (20)

<220>
<221> unsure
<222> (27)

<400> 99
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aaaaaaaaaa aaaaaaaaaa aaaaa 85

<210> 100
<211> 313
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (68)

<220>
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<222> (108)

<220>
<221> unsure
<222> (137)

<220>
<221> unsure
<222> (288)

<400> 100
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tggatttngt aaaggcaaaa acatttcttc ccattggcat acatcccntg tctctgcaca 120
atccttcttt gaaaatnaat atggtaactt aaatatattt agtacattac gttcctcttg 180
cttgtatcga catcattcaa aagctcttca aagcatttgt tcaaatcttc agtactggcc 240
agttttcata cagtctcggg gttttaaaac tttgaaatca aggacacnac gtctccagtc 300
tacctccgag aga 313

<210> 101
<211> 964
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (395)

<400> 101
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ggcctgaaag aagaagtgtg gaaattgata acaaaaacaa aaccatcaca gcatatcatg 180
aatctggtca tgccattatt gcatattaca caaaagatgc aatgcctatc aacaaagcta 240
caatcatgcc acgggggcca acacttggac atgtgtccct gttacctgag aatgacagat 300
ggaatgaaac tagagcccag ctgcttgcac aaatggatgt tagtatggga ggaagagtgg 360
cagaggagct tatatttgga accgaccata ttacnacagg tgcttccagt gattttgata 420
atgccactaa aatagcaaag cggatrgyta ccaaatttgg aatgagtgaa aagcttggag 480
ttatgaccta cagtgataca ggggaaacta agtccagaaa cccaatctgc catcgaacaa 540
gaaataagaa tccttctaag ggactcatat gaacgagcaa aacatatctt gaaaactcat 600
gcaaaggagc ataagaatct cgcagaagct ttattgacct atgagacttt ggatgccaaa 660
gagattcaaa ttgttctkga ggggaaaaag ttggaagtga gatgataact ctctkgatat 720
ggatgcttgc tggttttatt gcaagaatat aagtagcatt gcagtagtct acttttacaa 780
cgctttcccc tcattcttga tgtggtgtaa ttgaagggtg tgaaatgctt tgtcaatcat 840
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aaaa 964

<210> 102
<211> 166
<212> PRT
<213> Homo sapiens

<220>
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<222> (125)..(126)

<400> 102
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Gly Pro Glu Arg Arg Ser Val Glu Ile Asp Asn Lys Asn Lys Thr Ile
20 25 30

Thr Ala Tyr His Glu Ser Gly His Ala Ile Ile Ala Tyr Tyr Thr Lys
35 40 45

Asp Ala Met Pro Ile Asn Lys Ala Thr Ile Met Pro Arg Gly Pro Thr
50 55 60

Leu Gly His Val Ser Leu Leu Pro Glu Asn Asp Arg Trp Asn Glu Thr

65 70 75 80

Arg Ala Gln Leu Leu Ala Gln Met Asp Val Ser Met Gly Gly Arg Val
85 90 95

Ala Glu Glu Leu Ile Phe Gly Thr Asp His Ile Thr Thr Gly Ala Ser
100 105 110

Ser Asp Phe Asp Asn Ala Thr Lys Ile Ala Lys Arg Xaa Xaa Thr Lys
115 120 125

Phe Gly Met Ser Glu Lys Leu Gly Val Met Thr Tyr Ser Asp Thr Gly
130 135 140

Glu Thr Lys Ser Arg Asn Pro Ile Cys His Arg Thr Arg Asn Lys Asn
145 150 155 160

Pro Ser Lys Gly Leu Ile
165

<210> 103
<211> 1362
<212> DNA
<213> Homo sapiens

<400> 103
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tgaactcatg aatttaaaca tttgatgttg tttcagtcca ttgcagtcat tatccttatt 180
gattctcaaa gtgttttatt tttgacaaat aagttcttca aattagttag ttattttgat 240
agtgacctta atagtctttg ctagcttcca tccctgtatg gcataacaaa acattccagg 300
cccctttagt acatttcctg tcccagacct ggtattagtc atctaatctg gaagccctgc 360
tttctttctg tgggaaacat tatttcaaga cattagggat aagaatgcca gttgctactg 420
agttggttat tgtttcaagg atttatcaat acatagagca aataattatg ttttgctttg 480
tcttattttt atttctttac tttagaaaca gtacagctac ttacaaatca agtttagaac 540
tctcaggtta tcttaaatct gaagcttcta ccttcctaag aacaaaacac cggaatgatg 600
agatgtcata taaatatcca tttattttat ttcacaatac atacattgac ctattgtatg 660
tatgattagt acaaatggtt taaattggct tgttgtgctt tgttttgttt ttgcagtttt 720
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cacttgaagt agtttttctg tttgtagtaa tgttaccagt tggacacatt aggttcattt 840
atttttggga attgcttttg ttcccattta aatttttatt tatcttgcgt atcttggatt 900
aacggtaata gaccatatac aatttctct actttttttc attkgagagt ttcctcattt 960
attttgtttt cggatgcaaa gtatttcatt gtatgaatta ccagtttgtt caattagttt 1020
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actgaaagta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 1362

<210> 104
<211> 86
<212> PRT
<213> Homo sapiens

<400> 104
Met Pro Val Ala Thr Glu Leu Val Ile Val Ser Arg Ile Tyr Gln Tyr
1 5 10 15

Ile Glu Gln Ile Ile Met Phe Cys Phe Val Leu Phe Leu Phe Leu Tyr
20 25 30

Phe Arg Asn Ser Thr Ala Thr Tyr Lys Ser Ser Leu Glu Leu Ser Gly
35 40 45

Tyr Leu Lys Ser Glu Ala Ser Thr Phe Leu Arg Thr Lys His Arg Asn
50 55 60

Asp Glu Met Ser Tyr Lys Tyr Pro Phe Ile Leu Phe His Asn Thr Tyr
65 70 75 80

Ile Asp Leu Leu Tyr Val
85

<210> 105
<211> 479
<212> DNA
<213> Homo sapiens

<400> 105
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cccaaccttt gtcctcccca ctcttcgctc gcgcggcggt ctgagaccac caggaccagt 180
ttcaggggtt tccttctcca gcgagacttg gcagaacagg ctttaaaagc aaaggaggca 240
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caaataaaag atgggtggat tattttctcg atggaggaca aaaccttcaa ctgtagaagt 360
tctagaaagt atagataagg aaattcaagc attggaagaa tttagggaaa aaaaaaaaaa 420
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaa 479

<210> 106
<211> 33
<212> PRT
<213> Homo sapiens

<400> 106
Met Gly Gly Leu Phe Ser Arg Trp Arg Thr Lys Pro Ser Thr Val Glu
1 5 10 15

Val Leu Glu Ser Ile Asp Lys Glu Ile Gln Ala Leu Glu Glu Phe Arg
20 25 30

Glu

<210> 107
<211> 333
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (70)

<220>
<221> unsure
<222> (156)

<220>
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<220>
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<222> (207)

<220>
<221> unsure
<222> (308)

<400> 107
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agtggagaga ggccactccc tctccagccc ccgatntgga cccgggggag gggaggctga 180
tgcntttggc cccggcctgg ccaaaanagc ccatccccag ggcagtttca ggtgccggct 240
gggccctgaa tgtcaaggat aatatatagc ccgctcctgg gtcctggagc tgtggccctt 300
tgtactcntg ttgtgtccat tgtgtgtgtg cgt 333

<210> 108
<211> 611
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (62)

<220>
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<220>
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<220>
<221> unsure
<222> (290)

<400> 108
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gcccccctnt gctcagaatc tgaagtagtt ccctcctcag caatttcatn tcttgaacac 300
tgactcacac cttttaggca cctactgtgt gcatagcatt ccaccaggac tcatctccct 360
tccttctcag gggtcccga gccccgacta gctttgccct aactccttca tcaaaagacc 420
ccccgccagc ttcccacacc tcatacgcag ccacatctgc cctattctcc atgctttcca 480
gcttgcctgc ccttcctcat ctctccctgc ctgtgcagac ctccaccctt ctttcctcca 540
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ctgatcgtcc a 611

<210> 109
<211> 47

<212> PRT
<213> Homo sapiens

<400> 109
Met Leu Ser Ser Leu Pro Ala Leu Pro His Leu Ser Leu Pro Val Gln
1 5 10 15

Thr Ser Thr Leu Leu Ser Ser Thr Pro Pro Ser Pro Asn Ala Cys Arg
20 25 30

Pro Ser Ile His Ser Val Ser Ser Cys Val Val Ser Asp Arg Pro
35 40 45

<210> 110
<211> 274
<212> DNA
<213> Homo sapiens

<400> 110
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ttgagctgag cattctgctt gctgcagtag acgggtcgcc ttttgcccat accgaaattt 120
tctgaaatta aatcgcacac ccccaccatt tcctctcccc tgggatctgg aggaacatca 180
tacatagtag gtgaatcgtt ttgtagagtg aagaatgcta atgtaaagca aatagtcacc 240
cacgttccct tgtaaatcca aaaaaaaaaa aaaa 274

<210> 111
<211> 1646
<212> DNA
<213> Homo sapiens

<400> 111
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tattattatt gttgttgtta ctactattat ttttttttac ccaagggaga aagacaaaaa 120
aacggtggga tttatttaac atgatcttgg caaacgtctt ctgcctcttc ttctttctag 180
acgagaccct ccgctctttg gccagccctt cctccctgca gggccccgag ctccacggct 240
ggcgcccccc agtggactgt gtccgggcca atgagctgtg tgccgccgaa tccaactgca 300
gctctcgcta ccgcactctg cggcagtgcc tggcaggccg cgaccgcaac accatgctgg 360
ccaacaagga gtgccaggcg gccttggagg tcttgcagga gagcccgctg tacgactgcc 420
gctgcaagcg gggcatgaag aaggagctgc agtgtctgca gatctactgg agcatccacc 480
tggggctgac cgagggtgag gagttctacg aagcctcccc ctatgagccg gtgacctccc 540
gcctctcgga catcttcagg cttgcttcaa tcttctcagg gacaggggca gacccggtgg 600
tcagcgccaa gagcaaccat tgcctggatg ctgccaaggc ctgcaacctg aatgacaact 660
gcaagaagct gcgctcctcc tacatctcca tctgcaaccg cgagatctcg cccaccgagc 720
gctgcaaccg ccgcaagtgc cacaaggccc tgcgccagtt cttcgaccgg gtgcccagcg 780
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tgcgtggcgt gtgccggact gaccacctgt gtcggtcccg gctggccgac ttccatgcca 960
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cctttggcaa cggcacggac gtgaacgtgt ccccaaaagg cccctcgttc caggccaccc 1260
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acaaggtgat caaacctaac tcaggcccca gcagagccag accgtcggct gccttgaccg 1500
tgctgtctgt cctgatgctg aaacaggcct tgtaggctgt gggaaccgag tcagaagatt 1560
tttgaaagct acgcagacaa gaacagccgc ctgacgaaat ggaaacacac acagacacac 1620
acacaccttg caaaaaaaaa aaaaaa 1646

<210> 112
<211> 464
<212> PRT
<213> Homo sapiens

<400> 112
Met Ile Leu Ala Asn Val Phe Cys Leu Phe Phe Phe Leu Asp Glu Thr
1   5   10   15

Leu Arg Ser Leu Ala Ser Pro Ser Ser Leu Gln Gly Pro Glu Leu His
            20   25   30

Gly Trp Arg Pro Pro Val Asp Cys Val Arg Ala Asn Glu Leu Cys Ala
        35   40   45

Ala Glu Ser Asn Cys Ser Ser Arg Tyr Arg Thr Leu Arg Gln Cys Leu
    50   55   60

Ala Gly Arg Asp Arg Asn Thr Met Leu Ala Asn Lys Glu Cys Gln Ala
65   70   75   80

Ala Leu Glu Val Leu Gln Glu Ser Pro Leu Tyr Asp Cys Arg Cys Lys
                85   90   95

Arg Gly Met Lys Lys Glu Leu Gln Cys Leu Gln Ile Tyr Trp Ser Ile
            100   105   110

His Leu Gly Leu Thr Glu Gly Glu Glu Phe Tyr Glu Ala Ser Pro Tyr
        115   120   125

Glu Pro Val Thr Ser Arg Leu Ser Asp Ile Phe Arg Leu Ala Ser Ile
    130   135   140

Phe Ser Gly Thr Gly Ala Asp Pro Val Val Ser Ala Lys Ser Asn His
145   150   155   160

Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asn Asp Asn Cys Lys Lys
                165   170   175

Leu Arg Ser Ser Tyr Ile Ser Ile Cys Asn Arg Glu Ile Ser Pro Thr
            180   185   190

Glu Arg Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe
        195   200   205

Asp Arg Val Pro Ser Glu Tyr Thr Tyr Arg Met Leu Phe Cys Ser Cys
    210   215   220

Gln Asp Gln Ala Cys Ala Glu Arg Arg Arg Gln Thr Ile Leu Pro Ser
225   230   235   240

Cys Ser Tyr Glu Asp Lys Glu Lys Pro Asn Cys Leu Asp Leu Arg Gly
                245   250   255

Val Cys Arg Thr Asp His Leu Cys Arg Ser Arg Leu Ala Asp Phe His
            260   265   270

Ala Asn Cys Arg Ala Ser Tyr Gln Thr Val Thr Ser Cys Pro Ala Asp
        275   280   285

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Asn Tyr Gln Ala Cys Leu Gly Ser Tyr Ala Gly Met Ile Gly Phe Asp
    290                 295                 300

Met Thr Pro Asn Tyr Val Asp Ser Ser Pro Thr Gly Ile Val Val Ser
305                 310                 315                 320

Pro Trp Cys Ser Cys Arg Gly Ser Gly Asn Met Glu Glu Glu Cys Glu
                325                 330                 335

Lys Phe Leu Arg Asp Phe Thr Glu Asn Pro Cys Leu Arg Asn Ala Ile
            340                 345                 350

Gln Ala Phe Gly Asn Gly Thr Asp Val Asn Val Ser Pro Lys Gly Pro
        355                 360                 365

Ser Phe Gln Ala Thr Gln Ala Pro Arg Val Glu Lys Thr Pro Ser Leu
    370                 375                 380

Pro Asp Asp Leu Ser Asp Ser Thr Ser Leu Gly Thr Ser Val Ile Thr
385                 390                 395                 400

Thr Cys Thr Ser Val Gln Glu Gln Gly Leu Lys Ala Asn Asn Ser Lys
                405                 410                 415

Glu Leu Ser Met Cys Phe Thr Glu Leu Thr Thr Asn Ile Ile Pro Gly
            420                 425                 430

Ser Asn Lys Val Ile Lys Pro Asn Ser Gly Pro Ser Arg Ala Arg Pro
        435                 440                 445

Ser Ala Ala Leu Thr Val Leu Ser Val Leu Met Leu Lys Gln Ala Leu
    450                 455                 460
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<210> 113
<211> 355
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (133)

<220>
<221> unsure
<222> (151)

<220>
<221> unsure
<222> (196)

<220>
<221> unsure
<222> (228)

<400> 113
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tcttaaggaa acngacgtgc tcttctccgt ntaccagcac tcgggccgcc gagatccagt 180

cctgaggctt caccсntgga acaactgcac gcccctcaat cttgaagnga tctcctatgc 240
cgaccccact ccctcccgat ccctcagcag cagccccggg cacctccgag ttctggacat 300
cccccgatag cagcagcagc agcaggacgg gaaagaagcc ccacagagcg gccgc 355

<210> 114
<211> 587
<212> DNA
<213> Homo sapiens

<400> 114
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cagtcaatga atatgctgaa ttccaaccat gagttgcctg atgtttctga gttcatgaca 180
agactcttct cttcaaaatc atctggcaaa tctagcagcg gcagcagtaa aacaggcaaa 240
agtggggctg gcaaaaggag gtagtcaggc cgtccaragc tggcatttgc acaaacacgg 300
caacactggg tggcatccaa gtcttggaaa accgtgtgaa gcaactacta taaacttgag 360
tcatcccgac gttgatctct tacaactgtg tatgttaact ttttagcaca tgttttgtac 420
ttggtacacg agaaaaccca gctttcatct tttgtctgta tgaggtcaat attgatgtca 480
ctgaattaat tacagtgtcc tatagaaaat gccattaata aattatatga actactatac 540
attatgtata ttaattaaaa catcttaatc cagaaaaaaa aaaaaaa 587

<210> 115
<211> 81
<212> PRT
<213> Homo sapiens

<400> 115
Met Asn Pro Met Val Met Met Met Val Leu Pro Leu Leu Ile Phe Val
1   5   10   15

Leu Leu Pro Lys Val Val Asn Thr Ser Asp Pro Asp Met Arg Arg Glu
            20   25   30

Met Glu Gln Ser Met Asn Met Leu Asn Ser Asn His Glu Leu Pro Asp
        35   40   45

Val Ser Glu Phe Met Thr Arg Leu Phe Ser Ser Lys Ser Ser Gly Lys
    50   55   60

Ser Ser Ser Gly Ser Ser Lys Thr Gly Lys Ser Gly Ala Gly Lys Arg
65   70   75   80

Arg

<210> 116
<211> 601
<212> DNA
<213> Homo sapiens

<400> 116
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gcagtacgtg atcggcctgt tcctctcgtg cctctacacc atcttcctct tccccatcgg 180
ctttgtgggc aacatcctga tcctggtggt gaacatcagc ttccgcgaga agatgaccat 240
ccccgacctg tacttcatca acctggcggt ggcggacctc atcctggtgg ccgactccct 300
cattgaggtg ttcaacctgc acgagcggta ctacgacatc gccgtcctgt gcaccttcat 360
gtcgctcttc ctgcaggtca acatgtacag cagcgtcttc ttcctcacct ggatgagctt 420
cgaccgctac atcgccctgg ccagggccat gcgctgcagc ctgttccgca ccaagcacca 480

cgcccggctg agctgtggcc tcatctggat ggcatccgtg tcagccacgc tggtgccctt 540
caccgccgtg cacctgcagc acaccgacga ggcctgcttc tgtttcgcgg atgtccggga 600
g 601

<210> 117
<211> 200
<212> PRT
<213> Homo sapiens

<400> 117
Met Tyr Leu Gly Thr Ala Gln Pro Ala Ala Pro Asn Thr Thr Ser Pro
1 5 10 15

Glu Leu Asn Leu Ser His Pro Leu Leu Gly Thr Ala Leu Ala Asn Gly
20 25 30

Thr Gly Glu Leu Ser Glu His Gln Gln Tyr Val Ile Gly Leu Phe Leu
35 40 45

Ser Cys Leu Tyr Thr Ile Phe Leu Phe Pro Ile Gly Phe Val Gly Asn
50 55 60

Ile Leu Ile Leu Val Val Asn Ile Ser Phe Arg Glu Lys Met Thr Ile
65 70 75 80

Pro Asp Leu Tyr Phe Ile Asn Leu Ala Val Ala Asp Leu Ile Leu Val
85 90 95

Ala Asp Ser Leu Ile Glu Val Phe Asn Leu His Glu Arg Tyr Tyr Asp
100 105 110

Ile Ala Val Leu Cys Thr Phe Met Ser Leu Phe Leu Gln Val Asn Met
115 120 125

Tyr Ser Ser Val Phe Phe Leu Thr Trp Met Ser Phe Asp Arg Tyr Ile
130 135 140

Ala Leu Ala Arg Ala Met Arg Cys Ser Leu Phe Arg Thr Lys His His
145 150 155 160

Ala Arg Leu Ser Cys Gly Leu Ile Trp Met Ala Ser Val Ser Ala Thr
165 170 175

Leu Val Pro Phe Thr Ala Val His Leu Gln His Thr Asp Glu Ala Cys
180 185 190

Phe Cys Phe Ala Asp Val Arg Glu
195 200

<210> 118
<211> 419
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (80)

<220>

<221> unsure
<222> (178)

<400> 118
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gccgtctgct ccggggtggt tcagtcactg cttgttgaca tcaacatggc aattgcantc 180
atgtggactg ggaccgtgcg agctgccgtg tgggttagtc gggtgccagg acaatgaaat 240
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ggtgatgatg taaaaacctt cccataaaat gtaagaaaag ctgatgaggc tggtgacgtt 360
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<210> 119
<211> 714
<212> DNA
<213> Homo sapiens .

<220>
<221> unsure
<222> (646)

<220>
<221> unsure
<222> (649)

<400> 119
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tatctttctg cctcaagtac tggatgtgtt ttatgccaac atgaagaaaa gagaagggac 180
tcagctttct tcccaacagy ctartswtsy ytwwmyttky akcatttttg ggcttttcaa 240
agcaatctcc ccaaaaaaag aatcatttgg ttttggaaaa gaaaacagaa tcagcaactt 300
ttcgggtgtg tggtgaaaat gtcacgtgtg tggaatacgc tatctcctgg ctacaagacc 360
tgattgaaaa agaacagtgt ccttacacca gtgaagatga gtgcatcaaa gactttgatg 420
aaaaggagta tcaggagttg aatgagctgc agaagaagtt aaatattaac atttccctgg 480
accataagag acctttgatt aaggttttgg gaattagcag agatgtgatg caggctagag 540
atgaaattga ggcgatgatc aagagagttc gattggccaa agaacaggaa tcccgggcag 600
attgtatcag tgagtttata gaatggcagt ataatgacaa taacanttnt cattgtttta 660
acaaaatgac caatctgaaa ttagaggatg caaggagaga aaaaaaaaaa aaaa 714

<210> 120
<211> 159
<212> PRT
<213> Homo sapiens

<220>
<221> UNSURE
<222> (141)..(142)

<400> 120
Phe Leu Gly Phe Ser Lys Gln Ser Pro Gln Lys Lys Asn His Leu Val
1 5 10 15

Leu Glu Lys Lys Thr Glu Ser Ala Thr Phe Arg Val Cys Gly Glu Asn
20 25 30

Val Thr Cys Val Glu Tyr Ala Ile Ser Trp Leu Gln Asp Leu Ile Glu
35 40 45

Lys Glu Gln Cys Pro Tyr Thr Ser Glu Asp Glu Cys Ile Lys Asp Phe
50 55 60

Asp Glu Lys Glu Tyr Gln Glu Leu Asn Glu Leu Gln Lys Lys Leu Asn
65 70 75 80

Ile Asn Ile Ser Leu Asp His Lys Arg Pro Leu Ile Lys Val Leu Gly
85 90 95

Ile Ser Arg Asp Val Met Gln Ala Arg Asp Glu Ile Glu Ala Met Ile
100 105 110

Lys Arg Val Arg Leu Ala Lys Glu Gln Glu Ser Arg Ala Asp Cys Ile
115 120 125

Ser Glu Phe Ile Glu Trp Gln Tyr Asn Asp Asn Asn Xaa Xaa His Cys
130 135 140

Phe Asn Lys Met Thr Asn Leu Lys Leu Glu Asp Ala Arg Arg Glu
145 150 155

<210> 121
<211> 2681
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (2656)

<400> 121
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catgtgccga cctttcctgt ctcttttact ttgcagcacc aaatgctttc tactttgtgg 180
tctaggagga acacatgtca cttttgtaag ctgctcgaaa gcaggggcca caccttcatc 240
cttgttttcc acacaacacc aagcacttag tagacaccca ataaatcatt gctgaatgaa 300
tgtattcagc ctggaattgc actaggattt tttggccaac acattgtatt cttaactgat 360
accagacttc caatcaaata aaatccttaa gccttttcca tagtctttaa ttaaactact 420
tctcttccat tatttccctt tgcctacttt tgaactgata ttcagaactt ttctgttaat 480
gtttaatttt catccattat tcttgtctgt acagatcttt ttgatttttg actctcttat 540
ctagtttttt tttttttttt ttggcttccc gttgtgttat ccacaggcac aatgggtata 600
ttgactatcg ttcattgaag ttgttgatac aaatgttgaa caggagaaaa accagtagct 660
tgccaacttg gcacctcatt ctctagcttg acagtaatct cttatctagt agtttttaga 720
tatggttatt taatcaaata tcactagctt ctaattttgt tataattcat tcatgtatac 780
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ctgtcctgat tttgatttct gttaaactca gtaaacacat taccaaattt taaaataagg 2520
tgacttgttt tccccaactc acagttcacc aaaggtattt catctgtttg ttctgaaaat 2580
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tcatttcctt tgatgnaaaa aaaaaaaaaa aaaaaaaaaa a 2681

<210> 122
<211> 132
<212> PRT
<213> Homo sapiens

<400> 122
Met Glu Ala Val Arg Met Asn Trp Lys Glu Arg Leu Trp Glu Arg Gln
1 5 10 15

Arg Asp Glu Asn Lys Pro Gly Leu Ala Leu Pro Cys Ala His Thr Gly
20 25 30

Glu Leu Cys Ala Pro Gly Cys Val Ser Trp Tyr Met Arg Leu Ser Glu
35 40 45

Gly Ser Trp Gly Ala Leu Leu Ala Gln Arg Leu Arg Gly Arg Pro Arg
50 55 60

Lys Pro Phe Phe Ala Leu Val Arg Val Cys Cys Ile Phe Pro Ser Pro
65 70 75 80

Gly Asn Gly Thr Gln Phe Phe Phe Phe Leu Cys Lys Ile Ile Ser Ile
85 90 95

Thr Ile Gly Cys Ala His Glu Asn Ala Phe Cys Phe His Arg Asn Val
100 105 110

Phe Ser His Ser Val Leu Ile Leu Ile Ser Val Lys Leu Ser Lys His
115 120 125

Ile Thr Lys Phe
130

<210> 123
<211> 1585
<212> DNA
<213> Homo sapiens

<400> 123
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tactaaggat tgaggaccca aagatgaaca aaacatgggg cctaattcaa agatttcaca 180
atctggagag aaagtcagcc acatacaaaa aattataagg tagaatgtgc tataaaaaat 240

gatttaggta cagtggaagt ttagaaaggc ttcactaaag atgtcgtatt tgaattgggt 300
ctgagcatga attagtcttc aggtgaggga gggggttaaa gaaaactcta atgaaggaac 360
tctagtatgt gtgaaggcaa ggaggctggt gtgtttaggt tgcagcaaac caagtacaac 420
caggcttgga cttgagtgac tggaaagaca ggaagatgcc atgctgagaa aaactgccca 480
tgccaagctg agaaatgttc agcagaaaca taaggtgagc tgcatatgtc atttaaaatg 540
ttctaggagc cacattttta aaaaatcaaa attaacaagt caaaaaataa aaagcaatgg 600
ggggagatta aatgcatatt actaagtgaa agaagccaat ccaaaaaggc tacatacctg 660
tatgattcca actatatgac attctgaaaa aggccaaact atagagacag taaatgatca 720
gtggttgcca ggagttaggg aggagggagg gatgaacagg cagagcacag aagattttta 780
gagcagtaga actattttgt atgatattat aatattgtag atacatatca ttataaattt 840
gtccaaaccc atagaatgta caccaagagt gaactctaat gtaaactgtg gactttgggt 900
gataatgatg tgtcagtgta gattgatcag ttgtaacaaa tgtaccattc tggtggggaa 960
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caaattaatt ttaataatac attttattta acccaattta tcagaaatac taatatttta 1140
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ttgaaacagt aaaaaaaaaa aaaaa 1585

<210> 124
<211> 63
<212> PRT
<213> Homo sapiens

<400> 124
Met Leu Ser Leu Ile Arg Gly Tyr Val Asn Phe Pro Ala Phe Tyr Ser
1 5 10 15

Phe Ile Asn Leu Thr Ser Leu Ile Ala Tyr His Val Ser Gly Ser Val
20 25 30

Leu Arg Ile Glu Asp Pro Lys Met Asn Lys Thr Trp Gly Leu Ile Gln
35 40 45

Arg Phe His Asn Leu Glu Arg Lys Ser Ala Thr Tyr Lys Lys Leu
50 55 60

<210> 125
<211> 625
<212> DNA
<213> Homo sapiens

<400> 125
gatcccacca gttctgcctg gcttcctcca tccccagagg cactaaaagc agtattttaa 60
ggttggtgtc ttactccctg gaagcctgaa atgggtggaa tagcggtaag gcttgagtaa 120
aactagggga cagaggttct tatttgtcga ttttatttta taatttgacc acagcatctg 180
aactccctct ctccctggaa taagtatttt tcccacattt ttggatatat gtatggtaga 240
caattttttt ttaagacaca gagataaatg ttttcctgct ttggttacct ttcctttccc 300
ctttaaaagg aattagctat agaactgctt tgtaaagatg cttcttgata ttttactttt 360
gttccttttc cctaatcatt ccctttctc cccactcctc cagaaggcat aacccttctc 420
tccacacccc ctacccccac ccccgtccta ggctcccatc ctttccatca agaccttcat 480
tagcttatga tatttgctgc cgagatgtta taacaaggac tcgttcatgt atataagcta 540
tttcttgatc catttaaaag gaattgtaca ttgtgtagga aaaaaaaaaa aaaaaaaaaa 600
aaaaaaaaaa aaaaaaaaaa aaaaa 625

<210> 126
<211> 24
<212> PRT
<213> Homo sapiens

<400> 126
Met Leu Leu Asp Ile Leu Leu Leu Phe Leu Phe Pro Asn His Ser Leu
1   5   10   15

Phe Ser Pro Leu Leu Gln Lys Ala
            20

<210> 127
<211> 1946
<212> DNA
<213> Homo sapiens

<400> 127
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agggaagatg aagcctaaac tgatgtacca ggagctgaag gtgcctgcag aggagcccgc 180
caatgagctg cccatgaatg agattgaggc gtggaaggct gcggaaaaga aagcccgctg 240
ggtcctgctg gtcctcattc tggcggttgt gggcttcgga gccctgatga ctcagctgtt 300
tctatgggaa tacggcgact tgcatctctt tgggcccaac cagcgcccag ccccctgcta 360
tgacccttgc gaarcagtgc tggtggaaag cattcctgar ggcctggact tccccaatgc 420
ctccacgggg aacccttcca ccagccaggc ctggctgggc ctgctcgccg gtgcgcacag 480
cagcctggac atcgcctcct tctactggac cctcaccaac aatgacaccc acacgcagga 540
gccctctgcc cagcagggtg aggaggtcct ccggcagctg cagaccctgg caccaaaggg 600
cgtgaacgtc cgcatcgctg tgagcaagcc cagcgggccc cagccacagg cggacctgca 660
ggctctgctg cagagcggtg cccaggtccg catggtggac atgcagaagc tgacccatgg 720
cgtcctgcat accaagttct gggtggtgga ccagacccac ttctacctgg gcagtgccaa 780
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<210> 128
<211> 490
<212> PRT
<213> Homo sapiens

<220>

<221> UNSURE
<222> (83)

<220>
<221> UNSURE
<222> (480)

<220>
<221> UNSURE
<222> (482)

<220>
<221> UNSURE
<222> (490)

<400> 128
Met Lys Pro Lys Leu Met Tyr Gln Glu Leu Lys Val Pro Ala Glu Glu
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Pro Ala Asn Glu Leu Pro Met Asn Glu Ile Glu Ala Trp Lys Ala Ala
            20   25   30

Glu Lys Lys Ala Arg Trp Val Leu Leu Val Leu Ile Leu Ala Val Val
        35   40   45

Gly Phe Gly Ala Leu Met Thr Gln Leu Phe Leu Trp Glu Tyr Gly Asp
    50   55   60

Leu His Leu Phe Gly Pro Asn Gln Arg Pro Ala Pro Cys Tyr Asp Pro
65   70   75   80

Cys Glu Xaa Val Leu Val Glu Ser Ile Pro Glu Gly Leu Asp Phe Pro
                85   90   95

Asn Ala Ser Thr Gly Asn Pro Ser Thr Ser Gln Ala Trp Leu Gly Leu
            100   105   110

Leu Ala Gly Ala His Ser Ser Leu Asp Ile Ala Ser Phe Tyr Trp Thr
        115   120   125

Leu Thr Asn Asn Asp Thr His Thr Gln Glu Pro Ser Ala Gln Gln Gly
    130   135   140

Glu Glu Val Leu Arg Gln Leu Gln Thr Leu Ala Pro Lys Gly Val Asn
145   150   155   160

Val Arg Ile Ala Val Ser Lys Pro Ser Gly Pro Gln Pro Gln Ala Asp
                165   170   175

Leu Gln Ala Leu Leu Gln Ser Gly Ala Gln Val Arg Met Val Asp Met
            180   185   190

Gln Lys Leu Thr His Gly Val Leu His Thr Lys Phe Trp Val Val Asp
        195   200   205

Gln Thr His Phe Tyr Leu Gly Ser Ala Asn Met Asp Trp Arg Ser Leu
    210   215   220

Thr Gln Val Lys Glu Leu Gly Val Val Met Tyr Asn Cys Ser Cys Leu
225   230   235   240

Ala Arg Asp Leu Thr Lys Ile Phe Glu Ala Tyr Trp Phe Leu Gly Gln
245 250 255

Ala Gly Ser Ser Ile Pro Ser Thr Trp Pro Arg Phe Tyr Asp Thr Arg
260 265 270

Tyr Asn Gln Glu Thr Pro Met Glu Ile Cys Leu Asn Gly Thr Pro Ala
275 280 285

Leu Ala Tyr Leu Ala Ser Ala Pro Pro Pro Leu Cys Pro Ser Gly Arg
290 295 300

Thr Pro Asp Leu Lys Ala Leu Leu Asn Val Val Asp Asn Ala Arg Ser
305 310 315 320

Phe Ile Tyr Val Ala Val Met Asn Tyr Leu Pro Thr Leu Glu Phe Ser
325 330 335

His Pro His Arg Phe Trp Pro Ala Ile Asp Asp Gly Leu Arg Arg Ala
340 345 350

Thr Tyr Glu Arg Gly Val Lys Val Arg Leu Leu Ile Ser Cys Trp Gly
355 360 365

His Ser Glu Pro Ser Met Arg Ala Phe Leu Leu Ser Leu Ala Ala Leu
370 375 380

Arg Asp Asn His Thr His Ser Asp Ile Gln Val Lys Leu Phe Val Val
385 390 395 400

Pro Ala Asp Glu Ala Gln Ala Arg Ile Pro Tyr Ala Arg Val Asn His
405 410 415

Asn Lys Tyr Met Val Thr Glu Arg Ala Thr Tyr Ile Gly Thr Ser Asn
420 425 430

Trp Ser Gly Asn Tyr Phe Thr Glu Thr Ala Gly Thr Ser Leu Leu Val
435 440 445

Thr Gln Asn Gly Arg Gly Gly Leu Arg Ser Gln Leu Glu Ala Ile Phe
450 455 460

Leu Arg Asp Trp Asp Ser Pro Tyr Ser His Asp Leu Asp Thr Ser Xaa
465 470 475 480

Asp Xaa Val Gly Asn Ala Cys Arg Leu Xaa
485 490

<210> 129
<211> 6254
<212> DNA
<213> Homo sapiens

<400> 129
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cttagctgtt ggcattctcc tgagaaaagg atagcttcag aaatcagaaa aacatttggg 180
aggtgtctag cccagtggac cttctgaaga gcaatgctaa gaagacgttt ggtttaaaga 240

attaaaagga agaacaactt aagagcttct tcaaagttcc ccgcatgaaa attacttaaa 300
cgttgcacac aacgtttcac aaaatctttt gtgaaagaag aaaaggaaat tcagtgtgtg 360
agtctcagca ggagttaagc taatgcagct taacatcatg ccgacaaaga agcgcttatc 420
tgcgggcaga gtgcccctga ttctcttcct gtgccagatg attagtgcac tggaagtacc 480
tcttgatcca aaacttcttg aagacttggt acagcctcca accatcaccc aacagtctcc 540
aaaagattac attattgacc ctcgggagaa tattgtaatc cagtgtgaag ccaaagggaa 600
accgccccca agcttttcct ggacccgtaa tgggactcat tttgacatcg ataaagaccc 660
tctggtcacc atgaagcctg gcacaggaac gctcataatt aacatcatga gcgaagggaa 720
agctgagacc tatgaaggag tctatcagtg tacagcaagg aacgaacgcg gagctgcagt 780
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cattgcagaa ggactgccta ccccaattat ttactgggca aaggaagatg gaatgctacc 1260
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35 40 45

Thr Gln Gln Ser Pro Lys Asp Tyr Ile Ile Asp Pro Arg Glu Asn Ile
50 55 60

Val Ile Gln Cys Glu Ala Lys Gly Lys Pro Pro Pro Ser Phe Ser Trp
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Thr Arg Asn Gly Thr His Phe Asp Ile Asp Lys Asp Pro Leu Val Thr
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Met Lys Pro Gly Thr Gly Thr Leu Ile Ile Asn Ile Met Ser Glu Gly
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Lys Ala Glu Thr Tyr Glu Gly Val Tyr Gln Cys Thr Ala Arg Asn Glu
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Arg Gly Ala Ala Val Ser Asn Asn Ile Val Val Arg Pro Ser Arg Ser
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145 150 155 160

Gln Ser Leu Val Leu Pro Cys Arg Pro Pro Ile Gly Leu Pro Pro Pro
165 170 175

Ile Ile Phe Trp Met Asp Asn Ser Phe Gln Arg Leu Pro Gln Ser Glu
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Arg Val Ser Gln Gly Leu Asn Gly Asp Leu Tyr Phe Ser Asn Val Leu
195 200 205

Pro Glu Asp Thr Arg Glu Asp Tyr Ile Cys Tyr Ala Arg Phe Asn His
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Thr Gln Thr Ile Gln Gln Lys Gln Pro Ile Ser Val Lys Val Ile Ser
225 230 235 240

Ala Lys Ser Ser Arg Glu Arg Pro Pro Thr Phe Leu Thr Pro Glu Gly
245 250 255

Asn Ala Ser Asn Lys Glu Glu Leu Arg Gly Asn Val Leu Ser Leu Glu
260 265 270

Cys Ile Ala Glu Gly Leu Pro Thr Pro Ile Ile Tyr Trp Ala Lys Glu
275 280 285

Asp Gly Met Leu Pro Lys Asn Arg Thr Val Tyr Lys Asn Phe Glu Lys
290 295 300

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305 310 315 320

Cys Ile Ala Lys Asn Ala Leu Gly Ala Ile His His Thr Ile Ser Val
325 330 335

Arg Val Lys Ala Ala Pro Tyr Trp Ile Thr Ala Pro Gln Asn Leu Val
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355 360 365

Pro Lys Pro Arg Ile Ser Trp Leu Thr Asn Gly Val Pro Ile Glu Ile
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Asn Glu Tyr Gly Tyr Leu Leu Ala Asn Ala Phe Val Asn Val Leu Ala
            420                 425                 430

Glu Pro Pro Arg Ile Leu Thr Pro Ala Asn Thr Leu Tyr Gln Val Ile
        435                 440                 445

Ala Asn Arg Pro Ala Leu Leu Asp Cys Ala Phe Phe Gly Ser Pro Leu
    450                 455                 460

Pro Thr Ile Glu Trp Phe Lys Gly Ala Lys Gly Ser Ala Leu His Glu
465                 470                 475                 480

Asp Ile Tyr Val Leu His Glu Asn Gly Thr Leu Glu Ile Pro Val Ala
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Gln Lys Asp Ser Thr Gly Thr Tyr Thr Cys Val Ala Arg Asn Lys Leu
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Gly Met Ala Lys Asn Glu Val His Leu Glu Ile Lys Asp Ala Thr Trp
        515                 520                 525

Ile Val Lys Gln Pro Glu Tyr Ala Val Val Gln Arg Gly Ser Met Val
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Ser Phe Glu Cys Lys Val Lys His Asp His Thr Leu Ser Leu Thr Val
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Leu Trp Leu Lys Asp Asn Arg Glu Leu Pro Ser Asp Glu Arg Phe Thr
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Val Asp Lys Asp His Leu Val Val Ala Asp Val Ser Asp Asp Asp Ser
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Gly Thr Tyr Thr Cys Val Ala Asn Thr Thr Leu Asp Ser Val Ser Ala
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Ser Ala Val Leu Ser Val Val Ala Pro Thr Pro Thr Pro Ala Pro Val
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Tyr Asp Val Pro Asn Pro Pro Phe Asp Leu Glu Leu Thr Asp Gln Leu
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Asp Lys Ser Val Gln Leu Ser Trp Thr Pro Gly Asp Asp Asn Asn Ser
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Pro Ile Thr Lys Phe Ile Ile Glu Tyr Glu Asp Ala Met His Lys Pro
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Gly Leu Trp His His Gln Thr Glu Val Ser Gly Thr Gln Thr Thr Ala
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Gln Leu Lys Leu Ser Pro Tyr Val Asn Tyr Ser Phe Arg Val Met Ala
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Leu Thr Lys Ala Ser Glu Pro Asp Lys Asn Pro Thr Ala Val Glu Gly
725 730 735

Leu Gly Ser Glu Pro Asp Asn Leu Val Ile Thr Trp Lys Pro Leu Asn
740 745 750

Gly Phe Glu Ser Asn Gly Pro Gly Leu Gln Tyr Lys Val Ser Trp Arg
755 760 765

Gln Lys Asp Gly Asp Asp Glu Trp Thr Ser Val Val Val Ala Asn Val
770 775 780

Ser Lys Tyr Ile Val Ser Gly Thr Pro Thr Phe Val Pro Tyr Leu Ile
785 790 795 800

Lys Val Gln Ala Leu Asn Asp Met Gly Phe Ala Pro Glu Pro Ala Val
805 810 815

Val Met Gly His Ser Gly Glu Asp Leu Pro Met Val Ala Pro Gly Asn
820 825 830

Val Arg Val Asn Val Val Asn Ser Thr Leu Ala Glu Val His Trp Asp
835 840 845

Pro Val Pro Leu Lys Ser Ile Arg Gly His Leu Gln Gly Tyr Arg Ile
850 855 860

Tyr Tyr Trp Lys Thr Gln Ser Ser Ser Lys Arg Asn Arg Arg His Ile
865 870 875 880

Glu Lys Lys Ile Leu Thr Phe Gln Gly Ser Lys Thr His Gly Met Leu
885 890 895

Pro Gly Leu Glu Pro Phe Ser His Tyr Thr Leu Asn Val Arg Val Val
900 905 910

Asn Gly Lys Gly Glu Gly Pro Ala Ser Pro Asp Arg Val Phe Asn Thr
915 920 925

Pro Glu Gly Val Pro Ser Ala Pro Ser Ser Leu Lys Ile Val Asn Pro
930 935 940

Thr Leu Asp Ser Leu Thr Leu Glu Trp Asp Pro Pro Ser His Pro Asn
945 950 955 960

Gly Ile Leu Thr Glu Tyr Thr Leu Lys Tyr Gln Pro Ile Asn Ser Thr
965 970 975

His Glu Leu Gly Pro Leu Val Asp Leu Lys Ile Pro Ala Asn Lys Thr
980 985 990

Arg Trp Thr Leu Lys Asn Leu Asn Phe Ser Thr Arg Tyr Lys Phe Tyr
995 1000 1005

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Ala Gly Lys Ala Met Ala Ser Arg Gln Val Asp Ile Ala Thr Gln Gly
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Leu Ile Val Cys Phe Ile Arg Arg Asn Lys Gly Gly Lys Tyr Pro Val
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Lys Glu Lys Glu Asp Ala His Ala Asp Pro Glu Ile Gln Pro Met Lys
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Glu Asp Asp Gly Thr Phe Gly Glu Tyr Ser Asp Ala Glu Asp His Lys
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Pro Leu Lys Lys Gly Ser Arg Thr Pro Ser Asp Arg Thr Val Lys Lys
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Glu Asp Ser Asp Asp Ser Leu Val Asp Tyr Gly Glu Gly Val Asn Gly
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Glu Ser Asp Phe Asp Thr Met Pro Asp Ile Glu Ser Asp Lys Asn Ile
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Ile Arg Thr Lys Met Phe Leu Tyr Leu Ser Asp Leu Ser Arg Lys Asp
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Arg Arg Ile Val Ser Lys Lys Tyr Lys Ile Tyr Phe Trp Asn Ile Ile
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Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Ile Gln Leu Val Ile Thr
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Tyr Gln Thr Val Val Asn Val Thr Gly Asn Gln Asp Ile Cys Tyr Tyr
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Asn Phe Leu Cys Ala His Pro Leu Gly Val Leu Ser Ala Phe Asn Asn
130 135 140

Ile Leu Ser Asn Leu Gly His Val Leu Leu Gly Phe Leu Phe Leu Leu
145 150 155 160

Ile Val Leu Arg Arg Asp Ile Leu His Arg Arg Ala Leu Glu Ala Lys
165 170 175

Asp Ile Phe Ala Val Glu Tyr Gly Ile Pro Lys His Phe Gly Leu Phe
180 185 190

Tyr Ala Met Gly Ile Ala Leu Met Met Glu Gly Val Leu Ser Ala Cys
195 200 205

Tyr His Val Cys Pro Asn Tyr Ser Asn Phe Gln Phe Asp Thr Ser Phe
210 215 220

Met Tyr Met Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr Gln Thr Arg
225 230 235 240

His Pro Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala Ser Phe Ala
245 250 255

Val Val Ile Met Val Thr Val Leu Gly Val Val Phe Gly Lys Asn Asp
260 265 270

Val Trp Phe Trp Val Ile Phe Ser Ala Ile His Val Leu Ala Ser Leu
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Ala Leu Ser Thr Gln Ile Tyr Tyr Met Gly Arg Phe Lys Ile Asp Val
290 295 300

Ser Asp Thr Asp Leu Gly Ile Phe Arg Arg Ala Ala Met Val Phe Tyr
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Thr Asp Cys Ile Gln Gln Cys Ser Arg Pro Leu Tyr Met Asp Arg Met
325 330 335

Val Leu Leu Val Val Gly Asn Leu Val Asn Trp Ser Phe Ala Leu Phe
340 345 350

Gly Leu Ile Tyr Arg Pro Arg Asp Phe Ala Ser Tyr Met Leu Gly Ile
355 360 365

Phe Ile Cys Asn Leu Leu Leu Tyr Leu Ala Phe Tyr Ile Ile Met Lys
370 375 380

Leu Arg Ser Ser Glu Lys Val Leu Pro Val Pro Leu Phe Cys Ile Val
385 390 395 400

Ala Thr Ala Val Met Trp Ala Ala Ala Leu Tyr Phe Phe Phe Gln Asn
405 410 415

Leu Ser Ser Trp Glu Gly Thr Pro Ala Glu Ser Arg Glu Lys Asn Arg
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Glu Cys Ile Leu Leu Asp Phe Phe Asp Asp His Asp Ile Trp His Phe
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Asp Asn Leu Asp Ala Ile Leu Gly Asp Leu Thr Ser Ser Asp Phe Tyr
35 40 45

Asn Asn Ser Ile Ser Ser Asn Gly Ser His Leu Gly Thr Lys Gln Gln
50 55 60

Val Phe Gln Gly Thr Asn Ser Leu Gly Leu Lys Ser Ser Gln Ser Val
65 70 75 80

Gln Ser Ile Arg Pro Pro Tyr Asn Arg Ala Val Ser Leu Asp Ser Pro
85 90 95

Val Ser Val Gly Ser Ser Pro Pro Val Lys Asn Ile Ser Ala Phe Pro
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Met Leu Pro Lys Gln Pro Met Leu Gly Gly Asn Pro Arg Met Met Asp
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Ser Gln Glu Asn Tyr Gly Ser Ser Met Gly Asp Trp Gly Leu Pro Asn
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Ser Lys Ala
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<211> 119
<212> DNA
<213> Homo sapiens

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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaa 119

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<211> 3316
<212> DNA
<213> Homo sapiens

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<211> 547
<212> PRT
<213> Homo sapiens

<400> 137

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Gly Arg Tyr Pro Pro Trp Pro Gly Lys Ile Val Asn Pro Pro Lys Asp
            20                  25                  30

Leu Lys Lys Pro Arg Gly Lys Lys Cys Phe Phe Val Lys Phe Phe Gly
        35                  40                  45

Thr Glu Asp His Ala Trp Ile Lys Val Glu Gln Leu Lys Pro Tyr His
    50                  55                  60

Ala His Lys Glu Glu Met Ile Lys Ile Asn Lys Gly Lys Arg Phe Gln
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65 70 75 80

Gln Ala Val Asp Ala Val Glu Glu Phe Leu Arg Arg Ala Lys Gly Lys
85 90 95

Asp Gln Thr Ser Ser His Asn Ser Ser Asp Asp Lys Asn Arg Arg Asn
100 105 110

Ser Ser Glu Glu Arg Ser Arg Pro Asn Ser Gly Asp Glu Lys Arg Lys
115 120 125

Leu Ser Leu Ser Glu Gly Lys Val Lys Lys Asn Met Gly Glu Gly Lys
130 135 140

Lys Arg Val Ser Ser Gly Ser Ser Glu Arg Gly Ser Lys Ser Pro Leu
145 150 155 160

Lys Arg Ala Gln Glu Gln Ser Pro Arg Lys Arg Gly Arg Pro Pro Lys
165 170 175

Asp Glu Lys Asp Leu Thr Ile Pro Glu Ser Ser Thr Val Lys Gly Met
180 185 190

Met Ala Gly Pro Met Ala Ala Phe Lys Trp Gln Pro Thr Ala Ser Glu
195 200 205

Pro Val Lys Asp Ala Asp Pro His Phe His His Phe Leu Leu Ser Gln
210 215 220

Thr Glu Lys Pro Ala Val Cys Tyr Gln Ala Ile Thr Lys Lys Leu Lys
225 230 235 240

Ile Cys Glu Glu Glu Thr Gly Ser Thr Ser Ile Gln Ala Ala Asp Ser
245 250 255

Thr Ala Val Asn Gly Ser Ile Thr Pro Thr Asp Lys Lys Ile Gly Phe
260 265 270

Leu Gly Leu Gly Leu Met Gly Ser Gly Ile Val Ser Asn Leu Leu Lys
275 280 285

Met Gly His Thr Val Thr Val Trp Asn Arg Thr Ala Glu Lys Glu Gly
290 295 300

Ala Arg Leu Gly Arg Thr Pro Ala Glu Val Val Ser Thr Cys Asp Ile
305 310 315 320

Thr Phe Ala Cys Val Ser Asp Pro Lys Ala Ala Lys Asp Leu Val Leu
325 330 335

Gly Pro Ser Gly Val Leu Gln Gly Ile Arg Pro Gly Lys Cys Tyr Val
340 345 350

Asp Met Ser Thr Val Asp Ala Asp Thr Val Thr Glu Leu Ala Gln Val
355 360 365

Ile Val Ser Arg Gly Gly Arg Phe Leu Glu Ala Pro Val Ser Gly Asn
370 375 380

Gln Gln Leu Ser Asn Asp Gly Met Leu Val Ile Leu Ala Ala Gly Asp

385 390 395 400

Arg Gly Leu Tyr Glu Asp Cys Ser Ser Cys Phe Gln Ala Met Gly Lys
405 410 415

Thr Ser Phe Phe Leu Gly Glu Val Gly Asn Ala Ala Lys Met Met Leu
420 425 430

Ile Val Asn Met Val Gln Gly Ser Phe Met Ala Thr Ile Ala Glu Gly
435 440 445

Leu Thr Leu Ala Gln Val Thr Gly Gln Ser Gln Gln Thr Leu Leu Asp
450 455 460

Ile Leu Asn Gln Gly Gln Leu Ala Ser Ile Phe Leu Asp Gln Lys Cys
465 470 475 480

Gln Asn Ile Leu Gln Gly Asn Phe Lys Pro Asp Phe Tyr Leu Lys Tyr
485 490 495

Ile Gln Lys Asp Leu Arg Leu Ala Ile Ala Leu Gly Asp Ala Val Asn
500 505 510

His Pro Thr Pro Met Ala Ala Ala Ala Asn Glu Val Tyr Lys Arg Ala
515 520 525

Lys Ala Leu Asp Gln Ser Asp Asn Asp Met Ser Ala Val Tyr Arg Ala
530 535 540

Tyr Ile His
545

<210> 138
<211> 1097
<212> DNA
<213> Homo sapiens

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<210> 139

<211> 232
<212> PRT
<213> Homo sapiens

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Thr Asn Ala Ser Phe Thr Leu Gly His Gly Phe Gln Phe Val Ser Leu
            20   25   30

Ser Ser Pro Leu His Asn His Thr Leu Phe Pro Glu Lys Gln Ile Tyr
        35   40   45

Thr Thr Ser Pro Leu Glu Cys Gly Phe Gly Gln Ser Val Thr Ser Val
    50   55   60

Leu Pro Ser Ser Leu Pro Lys Pro Pro Phe Gly Met Leu Phe Gly Ser
65   70   75   80

Gln Pro Gly Leu Tyr Leu Ser Ala Leu Asp Ala Thr His Gln Gln Leu
                85   90   95

Thr Pro Ser Gln Glu Leu Asp Asp Leu Ile Asp Ser Gln Lys Asn Leu
            100   105   110

Glu Thr Ser Ser Ala Phe Gln Ser Ser Ser Gln Lys Leu Thr Ser Gln
        115   120   125

Lys Glu Gln Lys Asn Leu Glu Ser Ser Thr Gly Phe Gln Ile Pro Ser
    130   135   140

Gln Glu Leu Ala Ser Gln Ile Asp Pro Gln Lys Asp Ile Glu Pro Arg
145   150   155   160

Thr Thr Tyr Gln Ile Glu Asn Phe Ala Gln Ala Phe Gly Ser Gln Phe
                165   170   175

Lys Ser Gly Ser Arg Val Pro Met Thr Phe Ile Thr Asn Ser Asn Gly
            180   185   190

Glu Val Asp His Arg Val Arg Thr Ser Val Ser Asp Phe Ser Gly Tyr
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Thr Asn Met Met Ser Asp Val Ser Glu Pro Cys Ser Thr Arg Val Lys
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Thr Pro Thr Ser Gln Ser Tyr Arg
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<210> 140
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<212> DNA
<213> Homo sapiens

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aagtgctgca ttgtttttac aaataacagt ttgtagggaa aatatgacaa acctcaacta 420
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gctgtgaact tttttaaata agccatttag tgtgaaattg tcatgtatca aatggctatt 600
ggaaatggac tttactcaat tttaattcca ctgcactcta gccggagtga cagagtaaga 660
ctctgtctca aaaataaata aataaataaa taaataaata aataaataaa taaataaaaa 720
ataataatac aagttttcat aaggaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 775

<210> 141
<211> 44
<212> PRT
<213> Homo sapiens

<400> 141
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20 25 30

Ser Pro His Gln Arg His Leu Met Ile Tyr Leu Leu
35 40

<210> 142
<211> 2060
<212> DNA
<213> Homo sapiens

<400> 142
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<210> 143
<211> 62
<212> PRT
<213> Homo sapiens

<400> 143
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Glu Ile Ser Ala Arg His Phe Leu His Pro Phe Met Ala Ile Gln Arg
20 25 30

Ile Pro Leu Gln Lys Leu Leu Met Cys Tyr Phe Cys Cys Leu Val Met
35 40 45

Gln Ala Ala Leu Gly Pro Trp Val Thr Leu Pro Arg Leu Leu
50 55 60

<210> 144
<211> 1160
<212> DNA
<213> Homo sapiens

<400> 144
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<210> 145
<211> 309
<212> PRT
<213> Homo sapiens

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<221> UNSURE
<222> (152)

<400> 145
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Tyr Ile Arg Asp Trp Thr Ala His Arg Glu Glu Ile Ala Arg Ile Ser
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Gln Asp Leu Ala Leu Ile Ala Arg Glu Ile Asn Asp Val Ala Gly Glu
35 40 45

Ile Asp Ser Val Thr Ser Ser Gly Thr Ala Pro Ser Thr Thr Val Ser
50 55 60

Thr Ala Ala Thr Thr Pro Gly Ser Ala Ile Asp Thr Arg Glu Glu Leu
65 70 75 80

Val Asp Arg Val Phe Asp Glu Ser Leu Asn Phe Gln Lys Ile Pro Pro
85 90 95

Leu Val His Ser Lys Thr Pro Glu Gly Asn Asn Gly Arg Ser Gly Asp
100 105 110

Pro Arg Pro Gln Ala Ala Glu Pro Pro Asp His Leu Thr Ile Thr Arg
115 120 125

Arg Arg Thr Trp Ser Arg Asp Glu Val Met Gly Asp Asn Leu Leu Leu
130 135 140

Ser Ser Val Phe Gln Phe Ser Xaa Lys Ile Arg Gln Ser Ile Asp Lys
145 150 155 160

Thr Ala Gly Lys Ile Arg Ile Leu Phe Lys Asp Lys Asp Arg Asn Trp
165 170 175

Asp Asp Ile Glu Ser Lys Leu Arg Ala Glu Ser Glu Val Pro Ile Val
180 185 190

Lys Thr Ser Ser Met Glu Ile Ser Ser Ile Leu Gln Glu Leu Lys Arg
195 200 205

Val Glu Lys Gln Leu Gln Ala Ile Asn Ala Met Ile Asp Pro Asp Gly
210 215 220

Thr Leu Glu Ala Leu Asn Asn Met Gly Phe Pro Ser Ala Met Leu Pro
225 230 235 240

Ser Pro Pro Lys Gln Lys Ser Ser Pro Val Asn Asn His His Ser Pro
245 250 255

Gly Gln Thr Pro Thr Leu Gly Gln Pro Glu Ala Arg Ala Leu His Pro
260 265 270

Ala Ala Val Ser Ala Ala Ala Glu Phe Glu Asn Ala Glu Ser Glu Ala
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Asp Phe Ser Ile His Phe Asn Arg Val Asn Pro Asp Gly Glu Glu Glu

290 295 300

Asp Val Thr Val Thr
305

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<211> 1536
<212> DNA
<213> Homo sapiens

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<221> unsure
<222> (317)

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aggaacacca aaggtgcctg agatggcatg tgggggctgg gggcctgggg tctggggaat 900
ggagaggagc ctctctgtgc taacatttca gacctgccaa gagcaacaac ctagttagta 960
ccccagcagt acagaactca gtagtatggc tttgttgatc agtaatgact agcagggatg 1020
ttattacttc tgaatctaag tctgcacctg caagcagagt ttgataaatc cctcagtcag 1080
caaatcccct caaagccagg gcaagatata aataaaattc tatactagga atgagagcaa 1140
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ctaatctcca accttaggga gtaattatta ttatcccaat tttacagatc aaggaattgg 1260
actcaatagt taagtaactt agccaaggat gaacactcta tgcatagaac ttctgggaga 1320
gaaatgcttg ataccactta gtgtagctcc agcatggatc agcaaacttt ttctgtaaag 1380
aacaaaatgg taaatatttc aggttctgtg ggccagatgg cgtctgtagc aactacttaa 1440
ctgcggctgt ggcatgaaag cagccatgga tcatgtataa acaaatgggt gtggctgtgt 1500
accagtaaaa gtttatttag gaaaaaaaaa aaaaaa 1536

<210> 147
<211> 268
<212> PRT
<213> Homo sapiens

<220>
<221> UNSURE
<222> (67)

<400> 147
Met Lys Arg Thr His Leu Phe Ile Val Gly Ile Tyr Phe Leu Ser Ser
1 5 10 15

Cys Arg Ala Glu Glu Gly Leu Asn Phe Pro Thr Tyr Asp Gly Lys Asp
20 25 30

Arg Val Val Ser Leu Ser Glu Lys Asn Phe Lys Gln Val Leu Lys Lys

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        35                  40                  45

Tyr Asp Leu Leu Cys Leu Tyr Tyr His Glu Pro Val Ser Ser Asp Lys
    50                  55                  60

Val Thr Xaa Lys Gln Phe Gln Leu Lys Glu Ile Val Leu Glu Leu Val
65                  70                  75                  80

Ala His Val Leu Glu His Lys Ala Ile Gly Phe Val Met Val Asp Ala
                85                  90                  95

Lys Lys Glu Ala Lys Leu Ala Lys Lys Leu Gly Phe Asp Glu Glu Gly
            100                 105                 110

Ser Leu Tyr Ile Leu Lys Gly Asp Arg Thr Ile Glu Phe Asp Gly Glu
        115                 120                 125

Phe Ala Ala Asp Val Leu Val Glu Phe Leu Leu Asp Leu Ile Glu Asp
    130                 135                 140

Pro Val Glu Ile Ile Ser Ser Lys Leu Glu Val Gln Ala Phe Glu Arg
145                 150                 155                 160

Ile Glu Asp Tyr Ile Lys Leu Ile Gly Phe Phe Lys Ser Glu Asp Ser
                165                 170                 175

Glu Tyr Tyr Lys Ala Phe Glu Glu Ala Ala Glu His Phe Gln Pro Tyr
            180                 185                 190

Ile Lys Phe Phe Ala Thr Phe Asp Lys Gly Val Ala Lys Lys Leu Ser
        195                 200                 205

Leu Lys Met Asn Glu Val Asp Phe Tyr Glu Pro Phe Met Asp Glu Pro
    210                 215                 220

Ile Ala Ile Pro Asn Lys Pro Tyr Thr Glu Glu Glu Leu Val Glu Phe
225                 230                 235                 240

Val Lys Glu His Gln Arg Cys Leu Arg Trp His Val Gly Ala Gly Gly
                245                 250                 255

Leu Gly Ser Gly Glu Trp Arg Gly Ala Ser Leu Cys
            260                 265


<210> 148
<211> 1009
<212> DNA
<213> Homo sapiens

<400> 148
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ataagtgtcc aatcaaaaac tgtgtatttt tttaaatttg gaaaatactc aagttccagt 180
tgcttatcat tctccttcac tttctgaaaa cctggcaatc ccatgtggac ttctggtaga 240
atgagcaatg caaagaactg gcttggactt ggcatgtcct tgtacttctg ggggctgatg 300
gaccttacga ccaccgttct ctcggacacc ccaacaccac aaggtgaatt agaagcactc 360
ctgtcagaca agccacagtc acatcagcgg accaagarga gctgggtttg gaaccagttt 420
ttcgttctgg aagagtacac tgggaccgac cctttgtatg tcggcaaggt aagaaatgcc 480
aagtagaaat gacccgggta gtggatattg aaattgaata tgaattgagt atcaaagttg 540
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acctagcctt tatytgagac ctgagaaaaa ctagaacaag tggtacgtta cttgacacct 600
agctaaaatg taacttctgc tttgtcagag accagtctga aaggaaagat ttatttcctt 660
gtccatgtct ctggtatgaa tgggaaaaag tgggaattgg gatttggagg aaaaggctca 720
gaccctgcaa gagctattca agtcctaaaa gaggcagcag cagctgtctg ggaatgacag 780
aatgggggag agggaaactt ggaaatacaa gaagagtaca gagtttttg ctttgtgttt 840
ttatggggtt tttttcagag catttccaga ggtattgcct gaggtgcaaa tttaatgaaa 900
aaaataaaaa taaaacattt ttcatttcag aagatcttag catgtgcttt aggatagttg 960
gagacaataa atatatttat aaatgttaaa aaaaaaaaaa aaaaaaaaa 1009

<210> 149
<211> 87
<212> PRT
<213> Homo sapiens

<220>
<221> UNSURE
<222> (59)

<400> 149
Met Trp Thr Ser Gly Arg Met Ser Asn Ala Lys Asn Trp Leu Gly Leu
1 5 10 15

Gly Met Ser Leu Tyr Phe Trp Gly Leu Met Asp Leu Thr Thr Thr Val
20 25 30

Leu Ser Asp Thr Pro Thr Pro Gln Gly Glu Leu Glu Ala Leu Leu Ser
35 40 45

Asp Lys Pro Gln Ser His Gln Arg Thr Lys Xaa Ser Trp Val Trp Asn
50 55 60

Gln Phe Phe Val Leu Glu Glu Tyr Thr Gly Thr Asp Pro Leu Tyr Val
65 70 75 80

Gly Lys Val Arg Asn Ala Lys
85

<210> 150
<211> 2546
<212> DNA
<213> Homo sapiens

<400> 150
aaaagaaacc aaggaaattt gtatgataag gcaggtaaag tgaggaaaca tgcaactgaa 60
caggaaaaaa ctgaagaggg attaggccct aatataaaaa gcattgtcac catgttgatg 120
ctgatgctat tgatgatgtt tgctgtccac tgtacctggg tcacaagcaa tgcctactct 180
agtccaagtg tagtcctggc ctcatacaat catgatggca ccaggaatat cttagatgat 240
tttagagaag cttacttttg gctaaggcaa aatacagatg aacatgcacg agtaatgtct 300
tggtgggatt atggctatca gatagctgga atggctaata gaactacgtt ggtggataat 360
aacacctgga ataacagcca catagcactg gtgggaaaag ctatgtcttc taatgaaaca 420
gcagcctata aaatcatgag gactctagat gtagattatg ttttggttat ttttggaggg 480
gttattggct attctggtga tgatatcaac aaatttctct ggatggttag gatagctgaa 540
ggagaacatc ccaaagacat tcgggaaagt gactatttta ccccacaggg agaattccgt 600
gtagacaaag caggatcccc tactttgttg aattgcctta tgtataaaat gtcatactac 660
agatttggag aaatgcagct ggattttcgt acacccccag gttttgaccg aacacgtaat 720
gctgagattg gaaataagga cattaaattc aaacatttgg aagaagcctt tacatcagaa 780
cactggcttg ttaggatata taaagtaaaa gcacctgata acagggagac attagatcac 840
aaacctcgag tcaccaacat ttcccaaaa cagaagtatt tgtcaaagaa gactaccaaa 900
aggaagcgtg gctacattaa aataagctg gtttttaaga aaggcaagaa aatatctaag 960

aagactgttt aaatgcactg ttctggttcc taacttgaag cagttgtcct tgtgagaacc 1020
ggtctttgcc tttagctcat gtcgtgtttc acagcaaaga gggtacagaa ccatcactgg 1080
tccaggttaa tgtacaaaat tttctggcaa tgcctgatta aaaaaataaa attggcttgt 1140
tgagaacagc tgttttcgat ttctaatgtg aagcaagaca gagcactgct gtaaatgtct 1200
agcagcagat ttttttttta ttggtacata ttatccttca aatctgagaa tttggactaa 1260
ctgcaccaaa gaaccctcta atttggtccc tggcacatgc atacttgtca atgtttttat 1320
tctcttacaa gacctgcatt ttatttgaat tacccgaata gcaatatgta aaatacaagt 1380
gacaaaatgt gatgagagct tcttgaaccg gtaaactagt acaggtctga gaaagacata 1440
ttagaagaat cattatactt ccctgaatta tatttatttt catgtttctc taatgcaaag 1500
aatgtttcat caaatgtata ttttctgttg cttactgttt gctctgagaa gaagctgctg 1560
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tattactgct gttagcagtc gttttcacca ggtacttaca gagcagattt catacatcat 1680
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accaggacgg agttttggta tcttagtact gaagttagca ctatgtttac atgcaaaaga 1800
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agtgacaaaa gacttgtaac aactttgcct ggactttttt catttacaa cagttcatcc 1920
attcacaatg attttgttct ctgctccata ttttttaatc ccttaagcat ttgatgaaac 1980
actctttagt gctatatgca ttttcttact tttgttaaaa atgtgacaat tgtcaaaaaa 2040
tgcactaaaa tgtaaatgga gattgaacaa gttcactttc cagcttatag gcaactttat 2100
acagacttga acatttctc cagttgttta gtaaaagtga aagagaaagg gtttttcctg 2160
ccacaggata taactttttt ttatataaca agcataacac accactgctt ttggtggaaa 2220
agtgcagaat agtatgtacc ttttatgaag aaaaatgtaa tttacaatat tcagtgagaa 2280
tgttactgct gattttcttt tccaaggtgt agaatattct ttgatttata gaattcattt 2340
ttgacccaga tgatggttcc tttacagaac aataaaatgg ctgaacattt tcacaaatag 2400
agtgtaacga agtctggatt tctgatacct tgtcatttgg gggattttat tttactttgt 2460
tgctttaaaa ttcaatgcag agaagttgtt gactgtaggg gaaataaagt taattcaaat 2520
tttgaaaaaa aaaaaaaaaa aaaaaa 2546

<210> 151
<211> 286
<212> PRT
<213> Homo sapiens

<400> 151

Met Leu Met Leu Met Leu Leu Met Met Phe Ala Val His Cys Thr Trp
1 5 10 15

Val Thr Ser Asn Ala Tyr Ser Ser Pro Ser Val Val Leu Ala Ser Tyr
20 25 30

Asn His Asp Gly Thr Arg Asn Ile Leu Asp Asp Phe Arg Glu Ala Tyr
35 40 45

Phe Trp Leu Arg Gln Asn Thr Asp Glu His Ala Arg Val Met Ser Trp
50 55 60

Trp Asp Tyr Gly Tyr Gln Ile Ala Gly Met Ala Asn Arg Thr Thr Leu
65 70 75 80

Val Asp Asn Asn Thr Trp Asn Asn Ser His Ile Ala Leu Val Gly Lys
85 90 95

Ala Met Ser Ser Asn Glu Thr Ala Ala Tyr Lys Ile Met Arg Thr Leu
100 105 110

Asp Val Asp Tyr Val Leu Val Ile Phe Gly Gly Val Ile Gly Tyr Ser
115 120 125

Gly Asp Asp Ile Asn Lys Phe Leu Trp Met Val Arg Ile Ala Glu Gly
130 135 140

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Glu His Pro Lys Asp Ile Arg Glu Ser Asp Tyr Phe Thr Pro Gln Gly
145                 150                 155                 160

Glu Phe Arg Val Asp Lys Ala Gly Ser Pro Thr Leu Leu Asn Cys Leu
                165                 170                 175

Met Tyr Lys Met Ser Tyr Tyr Arg Phe Gly Glu Met Gln Leu Asp Phe
            180                 185                 190

Arg Thr Pro Pro Gly Phe Asp Arg Thr Arg Asn Ala Glu Ile Gly Asn
        195                 200                 205

Lys Asp Ile Lys Phe Lys His Leu Glu Glu Ala Phe Thr Ser Glu His
    210                 215                 220

Trp Leu Val Arg Ile Tyr Lys Val Lys Ala Pro Asp Asn Arg Glu Thr
225                 230                 235                 240

Leu Asp His Lys Pro Arg Val Thr Asn Ile Phe Pro Lys Gln Lys Tyr
                245                 250                 255

Leu Ser Lys Lys Thr Thr Lys Arg Lys Arg Gly Tyr Ile Lys Asn Lys
            260                 265                 270

Leu Val Phe Lys Lys Gly Lys Lys Ile Ser Lys Lys Thr Val
        275                 280                 285


<210> 152
<211> 4061
<212> DNA
<213> Homo sapiens

<400> 152
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gagattgctc agttgaaaaa ggatcaacgt aaaagagatc atcmacttag acttctggaa 180
gcccaaaaaa gaaaccaaga agtggttcta cgtcgcaaaa ctgaagaggt tacggctctt 240
cgtcggcaag taagacccat gtcagataaa gtggctggga aagttactcg gaagctgagt 300
tcatctgatg cacctgctca ggacacaggt tccagtgcag ctgctgtcga aacagatgca 360
tcaaggacag gagcccagca gaaaatgaga attcctgtgg cgagagtcca ggccttacca 420
acgccggcaa caaatggaaa caggaaaaaa tatcagagga aaggattgac tggccgagtg 480
tttatttcca agacagctcg catgaagtgg cagctccttg agcgcagggt cacagacatc 540
atcatgcaga agatgaccat ttccaacatg gaggcagata tgaatagact cctcaagcaa 600
cgggaggaac tcacaaaaag acgagagaaa ctttcaaaaa gaagggagaa gatagtcaag 660
gagaatggag agggagataa aaatgtggct aatatcaatg aagagatgga gtcactgact 720
gctaatatcg attacatcaa tgacagtatt tctgattgtc aggccaacat aatgcagatg 780
gaagaagcaa aggaagaagg tgagacattg gatgttactg cagtcattaa tgcctgcacc 840
cttacagaag cccgatacct gctagatcac ttcctgtcaa tgggcatcaa taagggtctt 900
caggctgccc agaaagaggc tcaaattaaa gtactggaag gtcgactcaa acaaacagaa 960
ataaccagtg ctacccaaaa ccagctctta ttccatatgt tgaaagagaa ggcagaatta 1020
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gaaaatgtag aggatagtac tgatgaggat gctcctttaa acagcccagg atcagaagga 1140
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cgaaggagaa ccaccactca gatggaattg ctgtatgcag atagcagtga actagcttca 1260
gacactagta caggagatgc ctccttgcct ggccctctca cacctgttgc agaagggcaa 1320
gagattggaa tgaatacaga gacaagtggt acttctgcta gggaaaaaga gctctctccc 1380
ccacctggct taccttctaa gataggcagc atttccaggc agtcatctct atcagaaaaa 1440
aaaattccag agccttctcc tgtaacaagg agaaaggcat atgagaaagc agaaaaatca 1500
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aaggccaagg aacaaaagca ctcagattct ggaacttcag aggctagtct ttcacctcct 1560
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cagggaaaca catcagttca gcaggataag tctgatgaaa gtgactcctc tctctcggag 1680
gtacacagca gatcctccag aaggggcata atcaacccat ttcctgcttc aaaaggaatc 1740
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aatctggtga ctgggcagga aataatgtca ctgggggtc atcccaacaa tgtcgtgtct 1920
gtaaaatact gtaattatac cagtttggtc ttcactgtat caacatctta tattaaggtg 1980
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cagatcaatc aaattgccct aaacccaact ggcaccttcc tctatgctgc ttctggaaat 2160
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aaatatatct gaattcaact gctgactata aatggtattc taataaaatt gtgtactatc 2940
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gagttgtttc tattatgacc atttaatttt gtttttattt aatagtagta tttccttccc 3600
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cctgaaaata tttgcttgta aatgaaaact tagctagggc ttaaataaac atgttgctat 3960
gaaatkraaa aaaaaaaaaa aaaaraaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4020
aaraaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a                     4061
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<210> 153
<211> 910
<212> PRT
<213> Homo sapiens

<220>
<221> UNSURE
<222> (43)

<400> 153

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Met Lys Lys Thr Lys Val Arg Leu Met Lys Gln Met Lys Glu Glu Gln
 1               5                  10                  15

Glu Lys Ala Arg Leu Thr Glu Ser Arg Arg Asn Arg Glu Ile Ala Gln
            20                  25                  30
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Leu Lys Lys Asp Gln Arg Lys Arg Asp His Xaa Leu Arg Leu Leu Glu
35 40 45

Ala Gln Lys Arg Asn Gln Glu Val Val Leu Arg Arg Lys Thr Glu Glu
50 55 60

Val Thr Ala Leu Arg Arg Gln Val Arg Pro Met Ser Asp Lys Val Ala
65 70 75 80

Gly Lys Val Thr Arg Lys Leu Ser Ser Ser Asp Ala Pro Ala Gln Asp
85 90 95

Thr Gly Ser Ser Ala Ala Ala Val Glu Thr Asp Ala Ser Arg Thr Gly
100 105 110

Ala Gln Gln Lys Met Arg Ile Pro Val Ala Arg Val Gln Ala Leu Pro
115 120 125

Thr Pro Ala Thr Asn Gly Asn Arg Lys Lys Tyr Gln Arg Lys Gly Leu
130 135 140

Thr Gly Arg Val Phe Ile Ser Lys Thr Ala Arg Met Lys Trp Gln Leu
145 150 155 160

Leu Glu Arg Arg Val Thr Asp Ile Ile Met Gln Lys Met Thr Ile Ser
165 170 175

Asn Met Glu Ala Asp Met Asn Arg Leu Leu Lys Gln Arg Glu Glu Leu
180 185 190

Thr Lys Arg Arg Glu Lys Leu Ser Lys Arg Arg Glu Lys Ile Val Lys
195 200 205

Glu Asn Gly Glu Gly Asp Lys Asn Val Ala Asn Ile Asn Glu Glu Met
210 215 220

Glu Ser Leu Thr Ala Asn Ile Asp Tyr Ile Asn Asp Ser Ile Ser Asp
225 230 235 240

Cys Gln Ala Asn Ile Met Gln Met Glu Glu Ala Lys Glu Glu Gly Glu
245 250 255

Thr Leu Asp Val Thr Ala Val Ile Asn Ala Cys Thr Leu Thr Glu Ala
260 265 270

Arg Tyr Leu Leu Asp His Phe Leu Ser Met Gly Ile Asn Lys Gly Leu
275 280 285

Gln Ala Ala Gln Lys Glu Ala Gln Ile Lys Val Leu Glu Gly Arg Leu
290 295 300

Lys Gln Thr Glu Ile Thr Ser Ala Thr Gln Asn Gln Leu Leu Phe His
305 310 315 320

Met Leu Lys Glu Lys Ala Glu Leu Asn Pro Glu Leu Asp Ala Leu Leu
325 330 335

Gly His Ala Leu Gln Asp Leu Asp Ser Val Pro Leu Glu Asn Val Glu
340 345 350

Asp Ser Thr Asp Glu Asp Ala Pro Leu Asn Ser Pro Gly Ser Glu Gly
355 360 365

Ser Thr Leu Ser Ser Asp Leu Met Lys Leu Cys Gly Glu Val Lys Pro
370 375 380

Lys Asn Lys Ala Arg Arg Arg Thr Thr Thr Gln Met Glu Leu Leu Tyr
385 390 395 400

Ala Asp Ser Ser Glu Leu Ala Ser Asp Thr Ser Thr Gly Asp Ala Ser
405 410 415

Leu Pro Gly Pro Leu Thr Pro Val Ala Glu Gly Gln Glu Ile Gly Met
420 425 430

Asn Thr Glu Thr Ser Gly Thr Ser Ala Arg Glu Lys Glu Leu Ser Pro
435 440 445

Pro Pro Gly Leu Pro Ser Lys Ile Gly Ser Ile Ser Arg Gln Ser Ser
450 455 460

Leu Ser Glu Lys Lys Ile Pro Glu Pro Ser Pro Val Thr Arg Arg Lys
465 470 475 480

Ala Tyr Glu Lys Ala Glu Lys Ser Lys Ala Lys Glu Gln Lys His Ser
485 490 495

Asp Ser Gly Thr Ser Glu Ala Ser Leu Ser Pro Pro Ser Ser Pro Pro
500 505 510

Ser Arg Pro Arg Asn Glu Leu Asn Val Phe Asn Arg Leu Thr Val Ser
515 520 525

Gln Gly Asn Thr Ser Val Gln Gln Asp Lys Ser Asp Glu Ser Asp Ser
530 535 540

Ser Leu Ser Glu Val His Ser Arg Ser Ser Arg Arg Gly Ile Ile Asn
545 550 555 560

Pro Phe Pro Ala Ser Lys Gly Ile Arg Ala Phe Pro Leu Gln Cys Ile
565 570 575

His Ile Ala Glu Gly His Thr Lys Ala Val Leu Cys Val Asp Ser Thr
580 585 590

Asp Asp Leu Leu Phe Thr Gly Ser Lys Asp Arg Thr Cys Lys Val Trp
595 600 605

Asn Leu Val Thr Gly Gln Glu Ile Met Ser Leu Gly Gly His Pro Asn
610 615 620

Asn Val Val Ser Val Lys Tyr Cys Asn Tyr Thr Ser Leu Val Phe Thr
625 630 635 640

Val Ser Thr Ser Tyr Ile Lys Val Trp Asp Ile Arg Asp Ser Ala Lys
645 650 655

Cys Ile Arg Thr Leu Thr Ser Ser Gly Gln Val Thr Leu Gly Asp Ala
660 665 670

Cys Ser Ala Ser Thr Ser Arg Thr Val Ala Ile Pro Ser Gly Glu Asn
675 680 685

Gln Ile Asn Gln Ile Ala Leu Asn Pro Thr Gly Thr Phe Leu Tyr Ala
690 695 700

Ala Ser Gly Asn Ala Val Arg Met Trp Asp Leu Lys Arg Phe Gln Ser
705 710 715 720

Thr Gly Lys Leu Thr Gly His Leu Gly Pro Val Met Cys Leu Thr Val
725 730 735

Asp Gln Ile Ser Ser Gly Gln Asp Leu Ile Ile Thr Gly Ser Lys Asp
740 745 750

His Tyr Ile Lys Met Phe Asp Val Thr Glu Gly Ala Leu Gly Thr Val
755 760 765

Ser Pro Thr His Asn Phe Glu Pro Pro His Tyr Asp Gly Ile Glu Ala
770 775 780

Leu Thr Ile Gln Gly Asp Asn Leu Phe Ser Gly Ser Arg Asp Asn Gly
785 790 795 800

Ile Lys Lys Trp Asp Leu Thr Gln Lys Asp Leu Leu Gln Gln Val Pro
805 810 815

Asn Ala His Lys Asp Trp Val Cys Ala Leu Gly Val Val Pro Asp His
820 825 830

Pro Val Leu Leu Ser Gly Cys Arg Gly Gly Ile Leu Lys Val Trp Asn
835 840 845

Met Asp Thr Phe Met Pro Val Gly Glu Met Lys Gly His Asp Ser Pro
850 855 860

Ile Asn Ala Ile Cys Val Asn Ser Thr His Ile Phe Thr Ala Ala Asp
865 870 875 880

Asp Arg Thr Val Arg Ile Trp Lys Ala Arg Asn Leu Gln Asp Gly Gln
885 890 895

Ile Ser Asp Thr Gly Asp Leu Gly Glu Asp Ile Ala Ser Asn
900 905 910

<210> 154
<211> 372
<212> DNA
<213> Homo sapiens

<400> 154
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caggatattt tagccaaaac atcagccaag ctgtctcgag ctgaacagcg aatgaataga 120
ttggatcagt gctattgtga aaggacttgc accatgaagg gaaccaccta ccgagaattt 180
gagtcctgga tagacggctg taagaactgc acatgcctga atggaaccat ccagtgtgaa 240
actctaatct gcccaaatcc tgactgccca cttaagtccg ctcttgcgta tgtggatggc 300
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gaaagaaata ca 372

<210> 155
<211> 761
<212> DNA
<213> Homo sapiens

<220>
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<222> (299)

<400> 155
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caaagtttgt aaaggttatg atttttgttt tgaaaggcat aactgcatgg agaattccat 180
ctgcagaaat ntgaatgaca gggctgtttg tagctgtcga gatggtttta gggtttttcg 240
agaggataat gcctactgtg aagacatnga tgagtgtgct gaagggcgcc attactgtng 300
tgaaaataca atgtgtgtca acaccccggg ttcttttatg tgcatctgca aaactggata 360
catcagaatt gatgattatt catgtacaga acatgatgag tgtatcacaa atcagcacag 420
ctgtgatgaa aatgctttat gcttcaacac tgttggagga cacaactgtg tttgcaagcc 480
gggctataca gggaatggaa cgacatgcaa agcattttgc aaagatggct gtaggaatgg 540
aggagcctgt attgccgcta atgtgtgtgc ctgcccacaa ggcttcactg gacccagctg 600
tgaaacggac attgatgaat gctctgatgg ttttgttcaa tgtgacagtc gtgctaattg 660
cattaacctg cctggatggt accactgtga gtgcagagat ggctaccatg acaatgggat 720
gttttcacca agtggagaat cgtgtgaaga tattgatgag t                     761
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<210> 156
<211> 240
<212> PRT
<213> Homo sapiens

<220>
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<222> (23)

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<221> UNSURE
<222> (51)

<220>
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<222> (76)

<220>
<221> UNSURE
<222> (87)

<400> 156
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Met Lys Phe Val Glu Ser Ser Gly Cys Pro Ala Leu Asp Cys Pro Glu
  1               5                  10                  15
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Ser His Gln Ile Thr Leu Xaa His Ser Cys Cys Lys Val Cys Lys Gly
            20                  25                  30

Tyr Asp Phe Cys Phe Glu Arg His Asn Cys Met Glu Asn Ser Ile Cys
        35                  40                  45

Arg Asn Xaa Asn Asp Arg Ala Val Cys Ser Cys Arg Asp Gly Phe Arg
    50                  55                  60

Val Phe Arg Glu Asp Asn Ala Tyr Cys Glu Asp Xaa Asp Glu Cys Ala
65                  70                  75                  80

Glu Gly Arg His Tyr Cys Xaa Glu Asn Thr Met Cys Val Asn Thr Pro
                85                  90                  95

Gly Ser Phe Met Cys Ile Cys Lys Thr Gly Tyr Ile Arg Ile Asp Asp
            100                 105                 110

Tyr Ser Cys Thr Glu His Asp Glu Cys Ile Thr Asn Gln His Ser Cys
        115                 120                 125

Asp Glu Asn Ala Leu Cys Phe Asn Thr Val Gly Gly His Asn Cys Val
    130                 135                 140

Cys Lys Pro Gly Tyr Thr Gly Asn Gly Thr Thr Cys Lys Ala Phe Cys
145                 150                 155                 160

Lys Asp Gly Cys Arg Asn Gly Gly Ala Cys Ile Ala Ala Asn Val Cys
                165                 170                 175

Ala Cys Pro Gln Gly Phe Thr Gly Pro Ser Cys Glu Thr Asp Ile Asp
            180                 185                 190

Glu Cys Ser Asp Gly Phe Val Gln Cys Asp Ser Arg Ala Asn Cys Ile
        195                 200                 205

Asn Leu Pro Gly Trp Tyr His Cys Glu Cys Arg Asp Gly Tyr His Asp
    210                 215                 220

Asn Gly Met Phe Ser Pro Ser Gly Glu Ser Cys Glu Asp Ile Asp Glu
225                 230                 235                 240


<210> 157
<211> 342
<212> DNA
<213> Homo sapiens

<400> 157
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atgttatgta cagtacactc tgaaaagaaa tctgaaacaa gttattgtaa tgataaaaat 180
aatgcacagg catggttact taatattttc taacaggaaa agtcatccct atttccttgt 240
tttactgcac ttaatattat ttggttgaat ttgttcagta taagttcgtt ccttgtgcaa 300
aattaaataa atatttttct taccttaaaa aaaaaaaaaa aa                    342

<210> 158
<211> 1445
<212> DNA
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<213> Homo sapiens

<400> 158
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aaccctcggt tcttcctgca atacagtgga tacaatttgt catggctact ctgagataag 180
accacttttt tatctgagct tctgtgacct gctcctggga ctttgctggc tcacggagac 240
acttctctat ggagcttcag tagcaaataa ggacatcatc tgctataacc tacaagcagt 300
tggacagata ttctacattt cctcatttct ctacaccgtc aattacatct ggtatttgta 360
cacagagctg aggatgaaac acacccaaag tggacagagc acatctccac tggtgataga 420
ttatacttgt cgattttgtc aaatggcctt tgttttctca agcctgatac ctctgctatt 480
gatgacacct gtattctgtc tgggaaatac tagtgaatgt ttccaaaact tcagtcagag 540
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caacacatct gtctgtagca cactttattt ttatggtatc gccattttcc tgggcagctt 660
tgtactcagc ctccttacca ttatggtctt acttatccga gcccagacat tgtataagaa 720
gtttgtgaag tcaactggct ttctggggag tgaacagtgg gcagtgattc acattgtgga 780
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ctattcaggg agaggaagac actttccatc tcagagatag actcgtgtta ccttgatgga 1380
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aaaaa 1445

<210> 159
<211> 245
<212> PRT
<213> Homo sapiens

<400> 159
Met Lys His Thr Gln Ser Gly Gln Ser Thr Ser Pro Leu Val Ile Asp
1 5 10 15

Tyr Thr Cys Arg Phe Cys Gln Met Ala Phe Val Phe Ser Ser Leu Ile
20 25 30

Pro Leu Leu Leu Met Thr Pro Val Phe Cys Leu Gly Asn Thr Ser Glu
35 40 45

Cys Phe Gln Asn Phe Ser Gln Ser His Asn Cys Ile Leu Met His Ser
50 55 60

Pro Pro Ser Ala Met Ala Glu Leu Pro Pro Ser Ala Asn Thr Ser Val
65 70 75 80

Cys Ser Thr Leu Tyr Phe Tyr Gly Ile Ala Ile Phe Leu Gly Ser Phe
85 90 95

Val Leu Ser Leu Leu Thr Ile Met Val Leu Leu Ile Arg Ala Gln Thr
100 105 110

Leu Tyr Lys Lys Phe Val Lys Ser Thr Gly Phe Leu Gly Ser Glu Gln
115 120 125

Trp Ala Val Ile His Ile Val Asp Gln Arg Val Arg Phe Tyr Pro Val

130 135 140

Ala Phe Phe Cys Cys Trp Gly Pro Ala Val Ile Leu Met Ile Ile Lys
145 150 155 160

Leu Thr Lys Pro Gln Asp Thr Lys Leu His Met Ala Leu Tyr Val Leu
165 170 175

Gln Ala Leu Thr Ala Thr Ser Gln Gly Leu Leu Asn Cys Gly Val Tyr
180 185 190

Gly Trp Thr Gln His Lys Phe His Gln Leu Lys Gln Glu Ala Arg Arg
195 200 205

Asp Ala Asp Thr Gln Thr Pro Leu Leu Cys Ser Gln Lys Arg Phe Tyr
210 215 220

Ser Arg Gly Leu Asn Ser Leu Glu Ser Thr Leu Thr Phe Pro Ala Ser
225 230 235 240

Thr Ser Thr Ile Phe
245

<210> 160
<211> 3550
<212> DNA
<213> Homo sapiens

<400> 160
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ctactatgag gtcagaagcc ttgctgctat atttcacact gctacacttt gctggggctg 180
gtttcccaga agattctgag ccaatcagta tttcgcatgg caactataca aaacagtatc 240
cggtgtttgt gggccacaag ccaggacgga acaccacaca gaggcacagg ctggacatcc 300
agatgattat gatcatgaac ggaaccctct acattgctgc tagggaccat atttatactg 360
ttgatataga cacatcacac acsgaagaaa tttattgtag caaaaaactg acatggaaat 420
ctagacaggc cgatgtagac acatgcagaa tgaagggaaa acataaggat gagtgccaca 480
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ccttcaaccc ttcctgcaga aactataaga tggatacatt ggaaccattc ggggatgaat 600
tcagcggaat ggccagatgc ccatatgatg ccaaacatgc caacgttgca ctgtttgcag 660
atggaaaact atactcagcc acagtgactg acttccttgc cattgacgca gtcatttacc 720
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aaccatactt tgttcaagcc gtggattacg gagattatat ctacttcttc ttcagggaaa 840
tagcagtgga gtataacacc atgggaaagg tagttttccc aagagtggct caggtttgta 900
agaatgatat gggaggatct caaagagtcc tggagaaaca gtggacgtcg ttcctgaagg 960
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cacagaggtg aacagaaact gaaacatttt gtccacaact tcacgggacg tggccagact 3480
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aaaaaaaaaa 3550

<210> 161
<211> 975
<212> PRT
<213> Homo sapiens

<400> 161
Met Arg Ser Glu Ala Leu Leu Leu Tyr Phe Thr Leu Leu His Phe Ala
1 5 10 15

Gly Ala Gly Phe Pro Glu Asp Ser Glu Pro Ile Ser Ile Ser His Gly
20 25 30

Asn Tyr Thr Lys Gln Tyr Pro Val Phe Val Gly His Lys Pro Gly Arg
35 40 45

Asn Thr Thr Gln Arg His Arg Leu Asp Ile Gln Met Ile Met Ile Met
50 55 60

Asn Gly Thr Leu Tyr Ile Ala Ala Arg Asp His Ile Tyr Thr Val Asp
65 70 75 80

Ile Asp Thr Ser His Thr Glu Glu Ile Tyr Cys Ser Lys Lys Leu Thr
85 90 95

Trp Lys Ser Arg Gln Ala Asp Val Asp Thr Cys Arg Met Lys Gly Lys
100 105 110

His Lys Asp Glu Cys His Asn Phe Ile Lys Val Leu Leu Lys Lys Asn
115 120 125

Asp Asp Ala Leu Phe Val Cys Gly Thr Asn Ala Phe Asn Pro Ser Cys
130 135 140

Arg Asn Tyr Lys Met Asp Thr Leu Glu Pro Phe Gly Asp Glu Phe Ser
145 150 155 160

Gly Met Ala Arg Cys Pro Tyr Asp Ala Lys His Ala Asn Val Ala Leu
165 170 175

Phe Ala Asp Gly Lys Leu Tyr Ser Ala Thr Val Thr Asp Phe Leu Ala
180 185 190

Ile Asp Ala Val Ile Tyr Arg Ser Leu Gly Glu Ser Pro Thr Leu Arg
195 200 205

Thr Val Lys His Asp Ser Lys Trp Leu Lys Glu Pro Tyr Phe Val Gln
210 215 220

Ala Val Asp Tyr Gly Asp Tyr Ile Tyr Phe Phe Phe Arg Glu Ile Ala
225 230 235 240

Val Glu Tyr Asn Thr Met Gly Lys Val Val Phe Pro Arg Val Ala Gln
245 250 255

Val Cys Lys Asn Asp Met Gly Gly Ser Gln Arg Val Leu Glu Lys Gln
260 265 270

Trp Thr Ser Phe Leu Lys Ala Arg Leu Asn Cys Ser Val Pro Gly Asp
275 280 285

Ser His Phe Tyr Phe Asn Ile Leu Gln Ala Val Thr Asp Val Ile Arg
290 295 300

Ile Asn Gly Arg Asp Val Val Leu Ala Thr Phe Ser Thr Pro Tyr Asn
305 310 315 320

Ser Ile Pro Gly Ser Ala Val Cys Ala Tyr Asp Met Leu Asp Ile Ala
325 330 335

Ser Val Phe Thr Gly Arg Phe Lys Glu Gln Lys Ser Pro Asp Ser Thr
340 345 350

Trp Thr Pro Val Pro Asp Glu Arg Val Pro Lys Pro Arg Pro Gly Cys
355 360 365

Cys Ala Gly Ser Ser Ser Leu Glu Arg Tyr Ala Thr Ser Asn Glu Phe
370 375 380

Pro Asp Asp Thr Leu Asn Phe Ile Lys Thr His Pro Leu Met Asp Glu
385 390 395 400

Ala Val Pro Ser Ile Phe Asn Arg Pro Trp Phe Leu Arg Thr Met Val
405 410 415

Arg Tyr Arg Leu Thr Lys Ile Ala Val Asp Thr Ala Ala Gly Pro Tyr
420 425 430

Gln Asn His Thr Val Val Phe Leu Gly Ser Glu Lys Gly Ile Ile Leu
435 440 445

```
Lys Phe Leu Ala Arg Ile Gly Asn Ser Gly Phe Leu Asn Asp Ser Leu
    450                 455                 460

Phe Leu Glu Glu Met Ser Val Tyr Asn Ser Glu Lys Cys Ser Tyr Asp
465                 470                 475                 480

Gly Val Glu Asp Lys Arg Ile Met Gly Met Gln Leu Asp Arg Ala Ser
                485                 490                 495

Ser Ser Leu Tyr Val Ala Phe Ser Thr Cys Val Ile Lys Val Pro Leu
            500                 505                 510

Gly Arg Cys Glu Arg His Gly Lys Cys Lys Lys Thr Cys Ile Ala Ser
        515                 520                 525

Arg Asp Pro Tyr Cys Gly Trp Ile Lys Glu Gly Gly Ala Cys Ser His
    530                 535                 540

Leu Ser Pro Asn Ser Arg Leu Thr Phe Glu Gln Asp Ile Glu Arg Gly
545                 550                 555                 560

Asn Thr Asp Gly Leu Gly Asp Cys His Asn Ser Phe Val Ala Leu Asn
                565                 570                 575

Gly Val Ile Arg Glu Ser Tyr Leu Lys Gly His Asp Gln Leu Val Pro
            580                 585                 590

Val Thr Leu Leu Ala Ile Ala Val Ile Leu Ala Phe Val Met Gly Ala
        595                 600                 605

Val Phe Ser Gly Ile Thr Val Tyr Cys Val Cys Asp His Arg Arg Lys
    610                 615                 620

Asp Val Ala Val Val Gln Arg Lys Glu Lys Glu Leu Thr His Ser Arg
625                 630                 635                 640

Arg Gly Ser Met Ser Ser Val Thr Lys Leu Ser Gly Leu Phe Gly Asp
                645                 650                 655

Thr Gln Ser Lys Asp Pro Lys Pro Glu Ala Ile Leu Thr Pro Leu Met
            660                 665                 670

His Asn Gly Lys Leu Ala Thr Pro Gly Asn Thr Ala Lys Met Leu Ile
        675                 680                 685

Lys Ala Asp Gln His His Leu Asp Leu Thr Ala Leu Pro Thr Pro Glu
    690                 695                 700

Ser Thr Pro Thr Leu Gln Gln Lys Arg Lys Pro Ser Arg Gly Ser Arg
705                 710                 715                 720

Glu Trp Glu Arg Asn Gln Asn Leu Ile Asn Ala Cys Thr Lys Asp Met
                725                 730                 735

Pro Pro Met Gly Ser Pro Val Ile Pro Thr Asp Leu Pro Leu Arg Ala
            740                 745                 750

Ser Pro Ser His Ile Pro Ser Val Val Val Leu Pro Ile Thr Gln Gln
        755                 760                 765
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Gly Tyr Gln His Glu Tyr Val Asp Gln Pro Lys Met Ser Glu Val Ala
770 775 780

Gln Met Ala Leu Glu Asp Gln Ala Ala Thr Leu Glu Tyr Lys Thr Ile
785 790 795 800

Lys Glu His Phe Ser Ser Lys Ser Pro Asn His Gly Val Asn Leu Val
805 810 815

Glu Asn Leu Asp Ser Leu Pro Pro Lys Val Pro Gln Arg Glu Ala Ser
820 825 830

Leu Gly Pro Pro Gly Ala Ser Leu Phe Gln Thr Gly Leu Ser Lys Arg
835 840 845

Leu Glu Met His His Ser Phe Ser Tyr Gly Val Asp Tyr Lys Arg Ser
850 855 860

Tyr Pro Thr Asn Ser Leu Thr Arg Ser His Gln Ala Thr Thr Leu Lys
865 870 875 880

Arg Asn Asn Thr Asn Ser Ser Asn Ser Ser His Leu Ser Arg Asn Gln
885 890 895

Ser Phe Gly Arg Gly Asp Asn Pro Pro Pro Ala Pro Gln Arg Val Asp
900 905 910

Ser Ile Gln Val His Ser Ser Gln Pro Ser Gly Gln Ala Val Thr Val
915 920 925

Ser Arg Gln Pro Ser Leu Asn Ala Tyr Asn Ser Leu Thr Arg Ser Gly
930 935 940

Leu Lys Arg Thr Pro Ser Leu Lys Pro Asp Val Pro Pro Lys Pro Ser
945 950 955 960

Phe Ala Pro Leu Ser Thr Ser Met Lys Pro Asn Asp Ala Cys Thr
965 970 975

<210> 162
<211> 1723
<212> DNA
<213> Homo sapiens

<400> 162
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actggagcag taggaggtgt ggggtcattt tatgaatata ataaaatgga gctgactatg 180
gacrrrgact wagtgtgggg gagaggggac gatacagggt gtgtgtctgg gagtgcctgg 240
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agagcccggt ggaagctact gttctctcca gtgtctcgag cgtagccaaa ataaggttgg 360
gaggctcccg gcctgtctgc tgtggtctga gctggctgca agcccaggtg ggggagcgag 420
tctgggaaga ttggctttga ctctctgttg ccagaggaga tgccatccca gcacggcccc 480
cactgtagtc caggctcgtg gtggcagcgg gggcaagggg aggggcaagg ctgccccccac 540
cccacgcacc aagtcacgcc aagtctcagc aggtaaaagc acgtgagcct agggcgagcg 600
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ccccagggca gggtcctacc tgggggtcag gagcaccttg gtcttgatga ttgattgatt 720
gatagaatgg agctgggtct gagcctccca ggcttgagct cctgggagtt cttgtgcggt 780

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catcagaggg agctgatgaa gaatggtccc tgtaagtaag tcactaggtt caacaactgc 900
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<210> 163
<211> 101
<212> PRT
<213> Homo sapiens

<220>
<221> UNSURE
<222> (49)

<220>
<221> UNSURE
<222> (51)

<220>
<221> UNSURE
<222> (81)

<400> 163

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Val Phe Arg Cys Pro Leu Leu Ile Gly Tyr Ile Asn Leu Leu Thr Leu
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Gly Val Thr Val Leu Ala Thr Phe Arg Gly Val Thr Gly Ala Val Gly
             20                  25                  30

Gly Val Gly Ser Phe Tyr Glu Tyr Asn Lys Met Glu Leu Thr Met Asp
         35                  40                  45

Xaa Asp Xaa Val Trp Gly Arg Gly Asp Asp Thr Gly Cys Val Ser Gly
     50                  55                  60

Ser Ala Trp Gly Thr Gly Thr Pro Arg Trp Ser Tyr Gly Arg Met Arg
 65                  70                  75                  80

Xaa Glu Gly Leu Gly Ser Pro Arg Ala Arg Trp Lys Leu Leu Phe Ser
                 85                  90                  95

Pro Val Ser Arg Ala
            100
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<210> 164
<211> 469
<212> DNA

<213> Homo sapiens

<400> 164
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tcgccccctc aaatcacccct ctccccgtagc ccacccgact aacatctcag tctctgaaaa 180
tgcacagaga tgcctggcta cctcgccctg ccttcagcct cacggggctc agtctctttt 240
tctctttggt gccaccagga cggagcatgg aggtcacagt acctgccacc ctcaacgtcc 300
tcaatggctc tgacgcccgc ctgccctgca ccttcaactc ctgctacaca gtgaaccaca 360
aacagttctc cctgaactgg acttaccagg agtgcaacaa ctgctctgag gagatgttcc 420
tccagttccg catgaagatc attaacctga agctggagcg gtttcaaga 469

<210> 165
<211> 96
<212> PRT
<213> Homo sapiens

<400> 165
Met His Arg Asp Ala Trp Leu Pro Arg Pro Ala Phe Ser Leu Thr Gly
1 5 10 15

Leu Ser Leu Phe Phe Ser Leu Val Pro Pro Gly Arg Ser Met Glu Val
20 25 30

Thr Val Pro Ala Thr Leu Asn Val Leu Asn Gly Ser Asp Ala Arg Leu
35 40 45

Pro Cys Thr Phe Asn Ser Cys Tyr Thr Val Asn His Lys Gln Phe Ser
50 55 60

Leu Asn Trp Thr Tyr Gln Glu Cys Asn Asn Cys Ser Glu Glu Met Phe
65 70 75 80

Leu Gln Phe Arg Met Lys Ile Ile Asn Leu Lys Leu Glu Arg Phe Gln
85 90 95

<210> 166
<211> 454
<212> DNA
<213> Homo sapiens

<400> 166
tggcttttgg ctacagagag ggaagggaaa gcctgaggcc ggcataaggg gaggccttgg 60
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aacaactcct ttggtgggga caaaagtgac aattgtaggc caggcacagt ggctcacgcc 180
tgtaatccca gcactttggg aggccaaggc gggtggatta cctccatctg tttagtagaa 240
atgggcaaaa ccccattttt actaaaaata caagaattag ctgggcgtgg tggcgtgtgc 300
ctgtaatccc agctatttgg gaggctgagg caggagaatc gcttgagccc gggaagcaga 360
ggttgcagtg aactgagata gtgatagtgc cactgcaatt cagcctgggt gacatagaga 420
gactccatct caaaaaaaaa aaaaaaaaaa aaaa 454

<210> 167
<211> 736
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (680)

<220>
<221> unsure
<222> (704)

<400> 167
gtttttaaac attatgttct acatgataaa tacatataat agtatgtcta tttaaataat 60
taaatttgaa aaaaactaat caaatattat cataagtaat gataaaaacc acaatttctt 120
ttgcagcaaa ctaataacac ctggatttct caatttatta agttgtactt acctgatgct 180
gatgatgatt actgtattta cacattgtct cagagctcac tcttgcggag gttgtggcct 240
cgaaaatgcc ttgttgtccc tctggaatct gtcttttcag cttcatctcc tcctcctcac 300
ctcctgctgt ggtgcacaga tacctatagg caggctccat ctcctcctcc ccagctcctc 360
ccctagtgca cagataccta taggcaggct tcatctcctc ctccccagct tctcccctag 420
tgcacagata cctataggca ggctccatct cctcctcccc agctcctccc ctartgcaca 480
gacacctata ggcaagctcc atctcctcct ctttagctag cctccccatc tcatcacaac 540
gcatgtctgt gacctttggt aatcatttac agtgccacac ggaaccctgt attttgcaca 600
cagcaaaaca aacaatgttt agctttattt atggtatttg atgactgtaa atggaaataa 660
atattgttct ttatttttn aaaaaaaaaa aaaaaaaaaa aaanaaaaaa aaaaaaaaaa 720
aaaaaaaaaa aaaaaa 736

<210> 168
<211> 114
<212> PRT
<213> Homo sapiens

<220>
<221> UNSURE
<222> (100)

<400> 168
Met Leu Met Met Ile Thr Val Phe Thr His Cys Leu Arg Ala His Ser
1 5 10 15

Cys Gly Gly Cys Gly Leu Glu Asn Ala Leu Leu Ser Leu Trp Asn Leu
20 25 30

Ser Phe Gln Leu His Leu Leu Leu Leu Thr Ser Cys Cys Gly Ala Gln
35 40 45

Ile Pro Ile Gly Arg Leu His Leu Leu Leu Pro Ser Ser Ser Pro Ser
50 55 60

Ala Gln Ile Pro Ile Gly Arg Leu His Leu Leu Leu Pro Ser Phe Ser
65 70 75 80

Pro Ser Ala Gln Ile Pro Ile Gly Arg Leu His Leu Leu Leu Pro Ser
85 90 95

Ser Ser Pro Xaa Ala Gln Thr Pro Ile Gly Lys Leu His Leu Leu Leu
100 105 110

Phe Ser

<210> 169
<211> 1427
<212> DNA
<213> Homo sapiens

<400> 169
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gcctcgacta agatttttct gatacctagt ttcacttttt aatgccctct gaaagttttt 120
tgatcagttg tttaatggga gatctgaaat gttaaactca gaccagaaag aagagaacct 180
gttttctaga aattaggttt ttaatccaag taagatgcaa gcttttgctt ttttaataac 240
ttgtatagct aaaaacttga cggtgaaaag ctctcagatc aaagctgatc cttctgtcag 300
taatgattct aaaaataagc aagattttaa tggggaatat attttatttc attcttatct 360
caaacctagg tactgtggtc gttttgagtt catttcgagg cattttcaat gtgcctcagg 420
ccacatccaa cctctyccca gggccagatt taatgttcag cctcataaag gttatcatag 480
ttttaacatt taagtactat tttgcagtgg gtatatacca aaatttgcta atagtaagat 540
aaccttagtt atatatcatt cacgttagtt ctatcttgga ggcaataaac atttcttgtt 600
caagaaattc atgttctatc ttggaggcaa taaacaaaca ttttttgttc aaaattaggg 660
ctaccctatt gtccttatgt cttttcctga tctgtggtca aacatttttc ttagtcattt 720
agaaattttc tatgttgttt taaatttttct ttaaatctag aatggagtat gtgaccaata 780
ctttcctttg gaatggtatg gacatttgaa atagagccca ttctttataa agtataaaat 840
atgtttaatg ctagtatttt taactaaact tttgagaaac tagattcaca tgctgttgta 900
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catacccact tcactcccat ccctactccc ttcttaaccc ttggcaacca taatctgttc 1140
tccattttta tagttttttt tttttcattt caataaagct gtataactgg aatcataata 1200
atatgtaacc ttttgggatt ggcttttttt catttagcat gattttctgg aggttaatcc 1260
agcttattat gtgtatcaag tctattgaca ggtacttttt agtgtgaata gaatcccata 1320
gtatagatgt accacagttt gtttaactgt tcacctgctg agagacattg ggccagtttt 1380
tggctactat aaataaagtt gctataaaca aaaaaaaaaa aaaaaaa 1427

<210> 170
<211> 79
<212> PRT
<213> Homo sapiens

<220>
<221> UNSURE
<222> (45)

<400> 170
Met Ile Leu Lys Ile Ser Lys Ile Leu Met Gly Asn Ile Phe Tyr Phe
1 5 10 15

Ile Leu Ile Ser Asn Leu Gly Thr Val Val Val Leu Ser Ser Phe Arg
20 25 30

Gly Ile Phe Asn Val Pro Gln Ala Thr Ser Asn Leu Xaa Pro Gly Pro
35 40 45

Asp Leu Met Phe Ser Leu Ile Lys Val Ile Ile Val Leu Thr Phe Lys
50 55 60

Tyr Tyr Phe Ala Val Gly Ile Tyr Gln Asn Leu Leu Ile Val Arg
65 70 75

<210> 171
<211> 572
<212> DNA
<213> Homo sapiens

<400> 171
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ttcttggcag ctgtagcagg ggccctggtc tatgctgaag atgcctcctc tgactcgacg 120

ggtgctgatc ctgcccagga agctgggacc tctaagccta atgaagagat ctcaggtcca 180
gcagaaccag cttcaccccc agagacaacc acaacagccc aggagacttc ggcggcagca 240
gttcagggga cagccaaggt cacctcaagc aggcaggaac taaacccct gaaatccata 300
gtggagaaaa gtatcttact aacagaacaa gcccttgcaa aagcaggaaa aggaatgcac 360
ggaggcgtgc caggtggaaa acaattcatc gaaaatggaa gtgaatttgc acaaaaatta 420
ctgaagaaat tcagtctatt aaaaccatgg gcatgagaag ctgaaaagaa tgggatcatt 480
ggacttaaag ccttaaatac ccttgtagcc cagagytatt aaaacgaaag catccaaaaa 540
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 572

<210> 172
<211> 138
<212> PRT
<213> Homo sapiens

<400> 172
Met Lys Phe Thr Thr Leu Leu Phe Leu Ala Ala Val Ala Gly Ala Leu
1 5 10 15

Val Tyr Ala Glu Asp Ala Ser Ser Asp Ser Thr Gly Ala Asp Pro Ala
20 25 30

Gln Glu Ala Gly Thr Ser Lys Pro Asn Glu Glu Ile Ser Gly Pro Ala
35 40 45

Glu Pro Ala Ser Pro Pro Glu Thr Thr Thr Thr Ala Gln Glu Thr Ser
50 55 60

Ala Ala Ala Val Gln Gly Thr Ala Lys Val Thr Ser Ser Arg Gln Glu
65 70 75 80

Leu Asn Pro Leu Lys Ser Ile Val Glu Lys Ser Ile Leu Leu Thr Glu
85 90 95

Gln Ala Leu Ala Lys Ala Gly Lys Gly Met His Gly Gly Val Pro Gly
100 105 110

Gly Lys Gln Phe Ile Glu Asn Gly Ser Glu Phe Ala Gln Lys Leu Leu
115 120 125

Lys Lys Phe Ser Leu Leu Lys Pro Trp Ala
130 135

<210> 173
<211> 1223
<212> DNA
<213> Homo sapiens

<400> 173
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tctggacttt ctttgctctt gtcttgtttt gggtgtactg gatcatgaca cttcttttc 120
ttggcactac cggcagtcct gttcagaatg agcaaggctt tgtggagttc aaaatttctg 180
ggcctctgca gtacatgtgg tggtaccatg tggtgggcct gatttggatc agtgaattta 240
ttctagcatg tcagcagatg acagtggcag gagctgtggt aacatactat tttactaggg 300
ataaaaggaa tttgccattt acacctattt tggcatcagt aaatcgcctt atycgttacc 360
acctaggtac ggtggcaaaa ggatctttca ttatcacatt agtcaaaatt ccgcgaatga 420
tccttatgta tattcacagt cagctcaaag gaaaggaaaa tgcttgtgca cgatgtgtgc 480
tgaaatcttg catttgttgc ctttggtgtc ttgaaaagtg cctaaattat ttaaatcaga 540
atgcatacac agccacagct atcaacagca ccaacttctg cacctcagca aaggatgcct 600
ttgtcattct ggtggagaat gctttgcgag tggctaccat caacacagta ggagatttta 660

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tgttattcct tggcaaggtg ctgatagtct gcagcacagg tttagctggg attatgctgc 720
tcaactacca gcaggactac acagtatggg tgctgcctct gatcatcgtc tgcctctttg 780
ctttcctagt cgctcattgc ttcctgtcta tttatgaaat ggtagtggat gtattattct 840
kgkgttttgc cattgawaca aaatacaatg atgggmgccc tggcagagaa ttctatatgg 900
ataaagtgct gatggagttt gtggaaaaca gtaggaaagc aatgaaagaa gctggtaagg 960
gaggcgtcgc tgattccaga gagctaaagc cgatgctgaa gaaaaggtga ctggtctcat 1020
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gttgagagtc tgcgattatg aagagcagga tcttattact tcaatgaaag catgtaacaa 1140
gtttctcaaa ccaccaacag ccaagtggat ttggtacagt gcggctgtct aataaataat 1200
caaaagcaaa aaaaaaaaaa aaa                                         1223
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<210> 174
<211> 301
<212> PRT
<213> Homo sapiens

<220>
<221> UNSURE
<222> (246)..(247)

<220>
<221> UNSURE
<222> (251)

<220>
<221> UNSURE
<222> (258)

<400> 174

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Met Thr Leu Leu Phe Leu Gly Thr Thr Gly Ser Pro Val Gln Asn Glu
1               5                   10                  15

Gln Gly Phe Val Glu Phe Lys Ile Ser Gly Pro Leu Gln Tyr Met Trp
            20                  25                  30

Trp Tyr His Val Val Gly Leu Ile Trp Ile Ser Glu Phe Ile Leu Ala
        35                  40                  45

Cys Gln Gln Met Thr Val Ala Gly Ala Val Val Thr Tyr Tyr Phe Thr
    50                  55                  60

Arg Asp Lys Arg Asn Leu Pro Phe Thr Pro Ile Leu Ala Ser Val Asn
65                  70                  75                  80

Arg Leu Ile Arg Tyr His Leu Gly Thr Val Ala Lys Gly Ser Phe Ile
                85                  90                  95

Ile Thr Leu Val Lys Ile Pro Arg Met Ile Leu Met Tyr Ile His Ser
            100                 105                 110

Gln Leu Lys Gly Lys Glu Asn Ala Cys Ala Arg Cys Val Leu Lys Ser
        115                 120                 125

Cys Ile Cys Cys Leu Trp Cys Leu Glu Lys Cys Leu Asn Tyr Leu Asn
    130                 135                 140

Gln Asn Ala Tyr Thr Ala Thr Ala Ile Asn Ser Thr Asn Phe Cys Thr
145                 150                 155                 160

Ser Ala Lys Asp Ala Phe Val Ile Leu Val Glu Asn Ala Leu Arg Val
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            165                 170                 175

Ala Thr Ile Asn Thr Val Gly Asp Phe Met Leu Phe Leu Gly Lys Val
        180                 185                 190

Leu Ile Val Cys Ser Thr Gly Leu Ala Gly Ile Met Leu Leu Asn Tyr
    195                 200                 205

Gln Gln Asp Tyr Thr Val Trp Val Leu Pro Leu Ile Ile Val Cys Leu
210                 215                 220

Phe Ala Phe Leu Val Ala His Cys Phe Leu Ser Ile Tyr Glu Met Val
225                 230                 235                 240

Val Asp Val Leu Phe Xaa Xaa Phe Ala Ile Xaa Thr Lys Tyr Asn Asp
            245                 250                 255

Gly Xaa Pro Gly Arg Glu Phe Tyr Met Asp Lys Val Leu Met Glu Phe
        260                 265                 270

Val Glu Asn Ser Arg Lys Ala Met Lys Glu Ala Gly Lys Gly Gly Val
    275                 280                 285

Ala Asp Ser Arg Glu Leu Lys Pro Met Leu Lys Lys Arg
290                 295                 300


<210> 175
<211> 2460
<212> DNA
<213> Homo sapiens

<400> 175
gagaagcgcg atgacggcta cgaggccgct gccagctcca aaactagctc aggcgatgcc 60
tcctcactca gcatcgaggg agactaacaa actccgggca aagttggggc tgaaaccctt 120
ggaggttaat gccatcaaga aggaggcggg caccaaggag gagcccgtga cagctgatgt 180
catcaaccct atggccttgc gacagcgaga ggagctgcgg gagaagctgg cggctgccaa 240
ggagaagcgc ctgctgaacc aaaagctggg gaagataaag accctaggag aggatgaccc 300
ctggctggac gacactgcag cctggatcga gaggagccgg cagctgcaga aggagaagga 360
cctggcagag aagagggcca agttactgga ggagatggac caaaagtttg gtgtcagcac 420
tctggtggag gaggagttcg ggcagaggcg gcaggacctg tacagtgccc gggacctgca 480
gggcctcact gtggagcatg ccattgattc cttccgagaa ggggagacaa tgattcttac 540
cctcaaggac aaaggcgtgc tgcaggagga ggaggacgtg ctggtgaacg tgaacctggt 600
ggataaggag cgggcagaga aaaatgtgga gctgcggaag aagaagcctg actacctgcc 660
ctatgccgag gacgagagcg tggacgacct ggcgcagcaa aaacctcgct ctatcctgtc 720
caagtatgac gaaaagcttg aaggggagcg gccacattcc ttccgcttgg agcagggcgg 780
cacggctgat ggcctgcggg agcgggagct ggaggagatc cgggccaagc tgcggctgca 840
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gatggtgacc tttaaaaaga ccaagcggag ggtgaagaaa atccgcaaga aggagaagga 960
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gcctgtgcct cagcccctgc cgtcggacga caccсgagtg gagaacatgg acatcagtga 1140
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cacgtccgag ttctgccgca ccttgggggа gatccccacc tacgggctgg ctggcaatcg 1440
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ctccgaatct gacggggagg agaacatcgg ctggagcacg gtgaacctgg acgaggagaa 1560
gcagcagcag gatgtgaggg ccacgccgct gggggtgggg cgtttggggg tgctcaagct 1620
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ggagatgagc accgggctcg gtgtccagag cctcagcctc ctcatccaga gtgggctctg 1680
cagacctccc agggcgatct gaggagtaaa tgaggaaatt aaatgttgtg gagggctggt 1740
gcctggcagg tggtgaccag tgggtggggc tgagaagagc cggtatggcc tgctaaccac 1800
ccccgccacg tgtcccgtag ttctctgctt cctccaccac catcctggac gaggaaccga 1860
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ccacagtgca gaaggtggcc cgggtgaagg cccccaacaa gtcgctgccc tcagccgtgt 1980
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ggatgagacg ggccggaaac tcacacccaa ggaggctttc cggcagctgt cgcaccgctt 2160
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<210> 176
<211> 563
<212> PRT
<213> Homo sapiens

<400> 176
Met Thr Ala Thr Arg Pro Leu Pro Ala Pro Lys Leu Ala Gln Ala Met
1 5 10 15

Pro Pro His Ser Ala Ser Arg Glu Thr Asn Lys Leu Arg Ala Lys Leu
20 25 30

Gly Leu Lys Pro Leu Glu Val Asn Ala Ile Lys Lys Glu Ala Gly Thr
35 40 45

Lys Glu Glu Pro Val Thr Ala Asp Val Ile Asn Pro Met Ala Leu Arg
50 55 60

Gln Arg Glu Glu Leu Arg Glu Lys Leu Ala Ala Ala Lys Glu Lys Arg
65 70 75 80

Leu Leu Asn Gln Lys Leu Gly Lys Ile Lys Thr Leu Gly Glu Asp Asp
85 90 95

Pro Trp Leu Asp Asp Thr Ala Ala Trp Ile Glu Arg Ser Arg Gln Leu
100 105 110

Gln Lys Glu Lys Asp Leu Ala Glu Lys Arg Ala Lys Leu Leu Glu Glu
115 120 125

Met Asp Gln Lys Phe Gly Val Ser Thr Leu Val Glu Glu Glu Phe Gly
130 135 140

Gln Arg Arg Gln Asp Leu Tyr Ser Ala Arg Asp Leu Gln Gly Leu Thr
145 150 155 160

Val Glu His Ala Ile Asp Ser Phe Arg Glu Gly Glu Thr Met Ile Leu
165 170 175

Thr Leu Lys Asp Lys Gly Val Leu Gln Glu Glu Glu Asp Val Leu Val
180 185 190

Asn Val Asn Leu Val Asp Lys Glu Arg Ala Glu Lys Asn Val Glu Leu
195 200 205

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Arg Lys Lys Lys Pro Asp Tyr Leu Pro Tyr Ala Glu Asp Glu Ser Val
    210                 215                 220

Asp Asp Leu Ala Gln Gln Lys Pro Arg Ser Ile Leu Ser Lys Tyr Asp
225                 230                 235                 240

Glu Lys Leu Glu Gly Glu Arg Pro His Ser Phe Arg Leu Glu Gln Gly
                245                 250                 255

Gly Thr Ala Asp Gly Leu Arg Glu Arg Glu Leu Glu Glu Ile Arg Ala
            260                 265                 270

Lys Leu Arg Leu Gln Ala Gln Ser Leu Ser Thr Val Gly Pro Arg Leu
        275                 280                 285

Ala Ser Glu Tyr Leu Thr Pro Glu Glu Met Val Thr Phe Lys Lys Thr
    290                 295                 300

Lys Arg Arg Val Lys Lys Ile Arg Lys Lys Glu Lys Glu Val Val Val
305                 310                 315                 320

Arg Ala Asp Asp Leu Leu Pro Leu Gly Asp Gln Thr Gln Asp Gly Asp
                325                 330                 335

Phe Gly Ser Arg Leu Arg Gly Arg Gly Arg Arg Arg Val Ser Glu Val
            340                 345                 350

Glu Glu Glu Lys Glu Pro Val Pro Gln Pro Leu Pro Ser Asp Asp Thr
        355                 360                 365

Arg Val Glu Asn Met Asp Ile Ser Asp Glu Glu Glu Gly Gly Ala Pro
    370                 375                 380

Pro Pro Gly Ser Pro Gln Val Leu Glu Glu Asp Glu Ala Glu Leu Glu
385                 390                 395                 400

Leu Gln Lys Gln Leu Glu Lys Gly Arg Arg Leu Arg Gln Leu Gln Gln
                405                 410                 415

Leu Gln Gln Leu Arg Asp Ser Gly Glu Lys Val Val Glu Ile Val Lys
            420                 425                 430

Lys Leu Glu Ser Arg Gln Arg Gly Trp Glu Glu Asp Glu Asp Pro Glu
        435                 440                 445

Arg Lys Gly Ala Ile Val Phe Asn Ala Thr Ser Glu Phe Cys Arg Thr
    450                 455                 460

Leu Gly Glu Ile Pro Thr Tyr Gly Leu Ala Gly Asn Arg Glu Glu Gln
465                 470                 475                 480

Glu Glu Leu Met Asp Phe Glu Arg Asp Glu Glu Arg Ser Ala Asn Gly
                485                 490                 495

Gly Ser Glu Ser Asp Gly Glu Glu Asn Ile Gly Trp Ser Thr Val Asn
            500                 505                 510

Leu Asp Glu Glu Lys Gln Gln Gln Asp Val Arg Ala Thr Pro Leu Gly
        515                 520                 525
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Gly Gly Arg Leu Gly Val Leu Lys Leu Glu Met Ser Thr Gly Leu Gly
530 535 540

Val Gln Ser Leu Ser Leu Leu Ile Gln Ser Gly Leu Cys Arg Pro Pro
545 550 555 560

Arg Ala Ile

<210> 177
<211> 1790
<212> DNA
<213> Homo sapiens

<400> 177
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agagacattt ccaattttca tgggagtcag taagatagag atgatgaaaa ttcagagtgt 180
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actcgtactc ttgtgaagtg ccctttagat actagtgtaa aatatactgc gtaattctcc 720
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gaacttgccc aggtatgagc cagcatttat taccactcat tctagaaggt gccagttagg 840
tagctatcca ggtttacatt ttaaggcagt cgagacctta ttcacgtggt atataaacaa 900
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gtacctctaa cagaaacttg tctttgcttc tgtctctctg ctactggact ctcagctcaa 1260
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agtagttaaa ctaaaattgc tactaacaca acattgtaga attcgttgcc ttaatggatg 1440
tgatcttcta ggcttactgt gtcttaacaa gcagtcttat atatatttat cttgcccaga 1500
aagtacactt gtagaattta acatttgctc ctttctccaa acagattaaa ggttatgcag 1560
ctgaatgatt ctgtgtccca ttttaaaggt ccaggctatc ccctagattt agattagttc 1620
ctaaaaaatc ttccagtctg aatcctgaca aatggatagc taaattaatt tccactcctc 1680
ttctctcttg cactgtttgg tacattacag ccaccattag ccttaaaagc tgcagcagcc 1740
aaattcggtg acagtaacat aaagcctgag cttaaaaaaa aaaaaaaaaa 1790

<210> 178
<211> 115
<212> PRT
<213> Homo sapiens

<400> 178
Met Glu Gln Asp Phe Ser Phe Ala Ala Gly Leu Leu Thr Ser Leu Cys
1 5 10 15

Phe Phe Phe Leu Arg Pro Phe Leu Ala Leu Ala Glu Leu Leu Pro Leu
20 25 30

Thr Ile Asn Leu Ser Asn Ser Ala Glu Ser Leu Gln Phe Thr Ala Leu

35 40 45

Asn Pro Ser Leu Gln Thr Lys Ala Asn Leu Met Ser Ser Asn Ser Tyr
50 55 60

Asn Ser Leu Leu Ser Gln Phe Arg Leu Gln Arg Leu His Leu Arg Gly
65 70 75 80

Asn Leu Lys Asn Lys Gln Cys Ser Ile Ser Val His Ile Lys Gly Thr
85 90 95

Ser Asn Arg Asn Leu Ser Leu Leu Leu Ser Leu Cys Tyr Trp Thr Leu
100 105 110

Ser Ser Arg
115

<210> 179
<211> 2026
<212> DNA
<213> Homo sapiens

<400> 179
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ccccaccatt gccctatggt gggcagatga attccagaaa ccctcaggga gccaggataa 180
ttaggcaacc catctgaatt ggccacgtaa gtgacaggca cttatctctc gggttcttgc 240
ttttgcagac tccagggaag tcctgtctag aggtcgatgg cagagactcc tactctttcc 300
catgaggggt tgataggaat caaattggga ttcctttggc tttgggtttt gttttttttgt 360
tgttgttttt ggttttcagt ttgttttttg gtgtatgggg ggtgattttg tttctgaata 420
agaaaaagaa gaggcaacca tggcccttat gtgggtttat ccttttttgag caatgtttta 480
gccacaagta aggaatcttg aaagtctttt gtccagcaag cagtcttaaa aatgtttttc 540
ctaactcctt ttgcaggtga ctaagtacaa aaaaatagtt ttctcattgt attcaaaata 600
gtgagtaggt tccctggata atacacagtg gtagttgaca tattttctca aaacacaacc 660
agaaaaccca cttccggtat ttgtaaatca cctttcaagg gaaaaagtga acacgtattc 720
cttgtatttc tagtttgatt accaaacctg atgttacaaa gaaacctccg ttctgtagac 780
agaatttctt ttatttttct tcttttactc ctcacaatca ctttcccagt gccatcacca 840
tctataaggt ctcagagcag aggattattc atggtaataa gtgggggtgt ggtgcagcca 900
ttccagtaac acccacaaga ggacagctgt tctgaatgtc cccacccacc cctctttcag 960
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tttctttggg gagaaatata tttacagatg gaagtgtgtg actgcgtgtc tgtgtgtgtg 1140
tgtggtgtgt gtgcgcacgt gagtgcgtgt gttcatctat gtgcatttca cttccataaa 1200
gacccagccc aagctgctgg gaaccatgtg ttcctgagta ttctcagagg ttaaacaagt 1260
gacaagtgag cttctgaaat tagtgtctca gcaagctggc tttaggaatg agccccattt 1320
tatcaagcag agaaaaaaaa taacagcaga aaagataaag ataaaccaaa aatatatacc 1380
ccccaatgga aaataatgtt gattcagcaa ttcccatagg atgtattaca tgctctaatt 1440
tattatatta ttatttatct gtctttgatc tttgcccatt gtactcttaa aagatgttg 1500
ggatgttgat tgcgattttt aaacaactag ataatgtata aatcagcagt ggaaatcagt 1560
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atttgtagta tttttaaaca tgaatgtcaa tttcaagtgt atttgaaatg gttcctccag 1740
gagagatatt tgtgcaccat taggaaaatc ttctctgcag aggaagtagc cttctttgga 1800
gaaaatggaa aatgggttct gatatgtgat ctcagagtag cccatttcct aggcaccat 1860
ggaaaacaca aatgtgatct ttaagtatac ctcttcccca gtttggggag gaaaggactc 1920
agtttgcacc cttttgtat gtaaaataaa atgtcttacc tttcttggct aaaaaaaaaa 1980
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2026

<210> 180

<211> 52
<212> PRT
<213> Homo sapiens

<400> 180
Met Leu Gln Arg Asn Leu Arg Ser Val Asp Arg Ile Ser Phe Ile Phe
1 5 10 15

Leu Leu Leu Leu Leu Thr Ile Thr Phe Pro Val Pro Ser Pro Ser Ile
20 25 30

Arg Ser Gln Ser Arg Gly Leu Phe Met Val Ile Ser Gly Gly Val Val
35 40 45

Gln Pro Phe Gln
50

<210> 181
<211> 1138
<212> DNA
<213> Homo sapiens

<400> 181
gggtctgtgg agagccgggt gcgagcggcg gcagcacgag gggaaaagag ctgagcggag 60
accaaagtca gccgggagac agtgggtctg tgagagaccg aatagagggg ctggggccac 120
gagcgccatt gacaagcaat ggggaagaaa cagaaaaaca agagcgaaga cagcaccaag 180
gatgacattg atcttgatgc cttggctgca gaaatagaag gagctggtgc tgccaaagaa 240
caggagcctc aaaagtcaaa agggaaaaag aaaaaagaga aaaaaaagca ggactttgat 300
gaagatgata tcctgaaaga actggaagaa ttgtctttgg aagctcaagg catcaaagct 360
gacagagaaa ctgttgcagt gaagccaaca gaaaacaatg aagaggaatt cacctcaaaa 420
gataaaaaaa agaaaggaca gaagggcaaa aaacagagtt ttgatgataa tgatagcgaa 480
gaattggaag ataaagattc aaaatcaaaa aagactgcaa aaccgaaagt ggaaatgtac 540
tctgggagtg atgatgatga tgattttaac aaacttccta aaaaagctaa agggaaagct 600
caaaaatcaa ataagaagtg ggatgggtca gaggaggatg aggataacag taaaaaaatt 660
aaagagcgtt caagaataaa ttcttctggt gaaagtggtg atgaatcaga tgaatttttg 720
caatctaaaa ggacagaaaa aaaatcagaa aaacaagcca ggtcctaaca tagaaagtgg 780
gaatgaagat gatgacgcct ccttcaaaat taagacagtg gccccaaaga aggcagaaaa 840
gaaggagcgc gagagaaaaa agcgagatga agaaaaagcg aaactgcgga agctgaaaga 900
aaaagaagag ttagaaacag gtaaaaagga tcagagtaaa caaaaggaat ctcaaaggaa 960
atttgaagaa gaaactgtaa aatccaaagt gactgttgat actggagtaa ttcctgcctc 1020
tgaagagaaa gcagagactc ccacagctgc agaagatgac aatgaaggag acaaaaagaa 1080
gaaagataag aagaaaaaga aaggagaaaa ggaagaaaaa gagaaaaaaa aaaaaaa 1138

<210> 182
<211> 209
<212> PRT
<213> Homo sapiens

<400> 182
Met Gly Lys Lys Gln Lys Asn Lys Ser Glu Asp Ser Thr Lys Asp Asp
1 5 10 15

Ile Asp Leu Asp Ala Leu Ala Ala Glu Ile Glu Gly Ala Gly Ala Ala
20 25 30

Lys Glu Gln Glu Prc Gln Lys Ser Lys Gly Lys Lys Lys Lys Glu Lys
35 40 45

Lys Lys Gln Asp Phe Asp Glu Asp Asp Ile Leu Lys Glu Leu Glu Glu

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    50                  55                  60

Leu Ser Leu Glu Ala Gln Gly Ile Lys Ala Asp Arg Glu Thr Val Ala
65                  70                  75                  80

Val Lys Pro Thr Glu Asn Asn Glu Glu Glu Phe Thr Ser Lys Asp Lys
                85                  90                  95

Lys Lys Lys Gly Gln Lys Gly Lys Lys Gln Ser Phe Asp Asp Asn Asp
            100                 105                 110

Ser Glu Glu Leu Glu Asp Lys Asp Ser Lys Ser Lys Lys Thr Ala Lys
        115                 120                 125

Pro Lys Val Glu Met Tyr Ser Gly Ser Asp Asp Asp Asp Asp Phe Asn
    130                 135                 140

Lys Leu Pro Lys Lys Ala Lys Gly Lys Ala Gln Lys Ser Asn Lys Lys
145                 150                 155                 160

Trp Asp Gly Ser Glu Glu Asp Glu Asp Asn Ser Lys Lys Ile Lys Glu
                165                 170                 175

Arg Ser Arg Ile Asn Ser Ser Gly Glu Ser Gly Asp Glu Ser Asp Glu
            180                 185                 190

Phe Leu Gln Ser Lys Arg Thr Glu Lys Lys Ser Glu Lys Gln Ala Arg
        195                 200                 205

Ser


<210> 183
<211> 912
<212> DNA
<213> Homo sapiens

<400> 183
atccagctct ttcagagaga agagatggga ataagataag aacatcattt cctgaagagt 60
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tgtgtgcacc tgtcctgcag tttgaggcag atgattttaa accagcatct atagacactt 180
cctgtgaagg agagcttcaa gttggcaaag gagatgaagt cacaattaca ctgccacata 240
tccctagctg agggcagcag taaaatccag gcccgaatgg aacagcagcc cactcgtcct 300
ccacagacgt cacagccacc accacctcca ccacctatgc cattcagagc tccaacgaag 360
cctccagttg gacccaaaac ttctcccttg aaagataacc cgtcacctga acctcagttg 420
gatgacatca aaagagagct gagggctgaa gttgacatta ttgaacaaat gagcagcagc 480
agtgggagca gctcttcaga ctctgagagc tcttcgggaa gtgatgacga tagctccagc 540
agtggaggsg aggamaatgg cccagcytct cytccgcagc yttmacacca gcagccytac 600
aacagtaggc ctgccgttgc caatggaacc agccggccac aaggaagcaa ccagytyatg 660
aacaccctca gaaatgactt gcagttgagt gagtytggca gtgacagtga tgactagtgc 720
tggatytttc gaaacctact ttttggtgca caaacatgcc gcaagactga gctactttgg 780
ccgtggagtc cattgcaaga ggaaaatgtt atggatcagt gactgtagta ggagtttgag 840
gctytggaac tctcacatat tcaagtcttt aacttagtgg tgatgggtga aaaaaaaaaa 900
aaaaaaaaaa aa                                                     912

<210> 184
<211> 167
<212> PRT
<213> Homo sapiens
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<220>
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<222> (114)

<220>
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<222> (120)

<220>
<221> UNSURE
<222> (123)..(124)

<220>
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<222> (148)

<220>
<221> UNSURE
<222> (161)

<400> 184
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Met Lys Ser Gln Leu His Cys His Ile Ser Leu Ala Glu Gly Ser Ser
  1               5                  10                  15

Lys Ile Gln Ala Arg Met Glu Gln Gln Pro Thr Arg Pro Pro Gln Thr
             20                  25                  30

Ser Gln Pro Pro Pro Pro Pro Pro Pro Met Pro Phe Arg Ala Pro Thr
         35                  40                  45

Lys Pro Pro Val Gly Pro Lys Thr Ser Pro Leu Lys Asp Asn Pro Ser
     50                  55                  60

Pro Glu Pro Gln Leu Asp Asp Ile Lys Arg Glu Leu Arg Ala Glu Val
 65                  70                  75                  80

Asp Ile Ile Glu Gln Met Ser Ser Ser Ser Gly Ser Ser Ser Ser Asp
                 85                  90                  95

Ser Glu Ser Ser Ser Gly Ser Asp Asp Asp Ser Ser Ser Ser Gly Gly
            100                 105                 110

Glu Xaa Asn Gly Pro Ala Ser Xaa Pro Gln Xaa Xaa His Gln Gln Pro
        115                 120                 125

Tyr Asn Ser Arg Pro Ala Val Ala Asn Gly Thr Ser Arg Pro Gln Gly
    130                 135                 140

Ser Asn Gln Xaa Met Asn Thr Leu Arg Asn Asp Leu Gln Leu Ser Glu
145                 150                 155                 160

Xaa Gly Ser Asp Ser Asp Asp
                165
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<210> 185
<211> 4582
<212> DNA
<213> Homo sapiens

<400> 185
ggtgaagcta atcaaatctg gttcctatgt agctctcact gttcagggac gcccacctgg 60
gtcgccccag attccacttg ccgactctga agtagagccg tcagtcattg gacatatgtc 120
tcccatcatg acatctcctc attcacctgg agcatctggg aatatggaga gaatcactag 180
tcctgtgctc atgggggagg aaaacaatgt ggttcataac cagaaagtag aaattctgag 240
aaaaatgtta cagaaagaac aggaacggct acagttattg caggaagatt acaaccgaac 300
acctgcccaa agattgctaa aagagatcca agaggccaag aaacacattc ctcagctgca 360
agagcagtta tccaaagcca caggctctgc tcaggatgga gctgtagtta caccctccag 420
acctttaggg gacaccctaa cagtcagtga ggcagaaaca gatcctggag atgtactggg 480
caggactgac tgtagcagtg gagatgcttc tcggcccagt agtgacaatg cagatagtcc 540
caagagtggc ccaaaagaga gaatttatct agaggaaaac ccagagaaaa gtgaaacaat 600
tcaggacact gacactcaat cacttgtcgg aagtccctca acccgtatag cacctcatat 660
tattggagca gaagatgatg attttggtac tgaacatgaa cagatcaatg gacagtgcag 720
ctgtttccag agcattgaat tactaaaatc tcgcccggct catttggctg ttttcttaca 780
ccatgtagtt tcacaatttg accctgcgac tttgctctgt tatctctatt cagacctgta 840
taaacatacc aattccaaag aaactcgtcg catcttcctt gagtttcatc agttctttct 900
aaatcgatca gcacacctga aagtttctgt tcctgatgaa atgtctgcag atctagaaaa 960
gagaagacct gagctcattc ctgaggatct gcatcgccac tatatccaaa ctatgcaaga 1020
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actgaccttg gctgaaagcg agctgactaa acttgatgca gagcgagaca aggaccgatt 1140
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ggtgactgaa catgggacac caaagccctt tcgaaagttt gacagtgtag cttttggaga 1860
aagtcaaagt gaggatgaac aatttgaaaa tgacttagag acagatccac ccaactggca 1920
gcagcttgtt agtcgagaag tgttactggg actaaaacct tgtgaaatca aaagacagga 1980
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ggctgcatca gtgaaggagc aatccacaaa gccgattcca ttaccacagt caacacctgg 3060
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ggatgcacta agaaatttgg gtttgttgaa gcagttgctg gtgcaacagc taggtttgac 3420
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gccgcagaca gacagtgtca tccagaactc tgaaaatatt aaggcctatc attctggtga 3540
aggacatatg ccctttagaa ctggaactgg tgacattgca acttgttaca gtccacggac 3600
ttcaactgaa tcttttgctc cacgggattc agtgggactg gcaccccagg atagccaggc 3660
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cacccaccag cagcaacatt ctcctcagaa tactcactcc gatggggcaa tttcaccatt 4020
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atttaagaaa aaaaaaaaaa aa 4582

<210> 186
<211> 1461
<212> PRT
<213> Homo sapiens

<220>
<221> UNSURE
<222> (364)

<220>
<221> UNSURE
<222> (369)

<220>
<221> UNSURE
<222> (1433)

<400> 186
Met Ser Pro Ile Met Thr Ser Pro His Ser Pro Gly Ala Ser Gly Asn
1 5 10 15

Met Glu Arg Ile Thr Ser Pro Val Leu Met Gly Glu Glu Asn Asn Val
20 25 30

Val His Asn Gln Lys Val Glu Ile Leu Arg Lys Met Leu Gln Lys Glu
35 40 45

Gln Glu Arg Leu Gln Leu Leu Gln Glu Asp Tyr Asn Arg Thr Pro Ala
50 55 60

Gln Arg Leu Leu Lys Glu Ile Gln Glu Ala Lys Lys His Ile Pro Gln
65 70 75 80

Leu Gln Glu Gln Leu Ser Lys Ala Thr Gly Ser Ala Gln Asp Gly Ala
85 90 95

Val Val Thr Pro Ser Arg Pro Leu Gly Asp Thr Leu Thr Val Ser Glu
100 105 110

Ala Glu Thr Asp Pro Gly Asp Val Leu Gly Arg Thr Asp Cys Ser Ser

115 120 125

Gly Asp Ala Ser Arg Pro Ser Ser Asp Asn Ala Asp Ser Pro Lys Ser
130 135 140

Gly Pro Lys Glu Arg Ile Tyr Leu Glu Glu Asn Pro Glu Lys Ser Glu
145 150 155 160

Thr Ile Gln Asp Thr Asp Thr Gln Ser Leu Val Gly Ser Pro Ser Thr
165 170 175

Arg Ile Ala Pro His Ile Ile Gly Ala Glu Asp Asp Asp Phe Gly Thr
180 185 190

Glu His Glu Gln Ile Asn Gly Gln Cys Ser Cys Phe Gln Ser Ile Glu
195 200 205

Leu Leu Lys Ser Arg Pro Ala His Leu Ala Val Phe Leu His His Val
210 215 220

Val Ser Gln Phe Asp Pro Ala Thr Leu Leu Cys Tyr Leu Tyr Ser Asp
225 230 235 240

Leu Tyr Lys His Thr Asn Ser Lys Glu Thr Arg Arg Ile Phe Leu Glu
245 250 255

Phe His Gln Phe Phe Leu Asn Arg Ser Ala His Leu Lys Val Ser Val
260 265 270

Pro Asp Glu Met Ser Ala Asp Leu Glu Lys Arg Arg Pro Glu Leu Ile
275 280 285

Pro Glu Asp Leu His Arg His Tyr Ile Gln Thr Met Gln Glu Arg Val
290 295 300

His Pro Glu Val Gln Arg His Leu Lys Asp Phe Arg Gln Lys Arg Ser
305 310 315 320

Met Gly Leu Thr Leu Ala Glu Ser Glu Leu Thr Lys Leu Asp Ala Glu
325 330 335

Arg Asp Lys Asp Arg Leu Thr Leu Glu Lys Glu Arg Thr Cys Ala Glu
340 345 350

Gln Ile Val Ala Lys Ile Glu Glu Val Leu Met Xaa Ala Gln Ala Val
355 360 365

Xaa Glu Asp Lys Ser Ser Thr Met Gln Tyr Val Ile Leu Met Tyr Met
370 375 380

Lys His Leu Gly Val Lys Val Lys Glu Pro Arg Asn Leu Glu His Lys
385 390 395 400

Arg Gly Arg Ile Gly Phe Leu Pro Lys Ile Lys Gln Ser Met Lys Lys
405 410 415

Asp Lys Glu Gly Glu Glu Lys Gly Lys Arg Arg Gly Phe Pro Ser Ile
420 425 430

Leu Gly Pro Pro Arg Arg Pro Ser Arg His Asp Asn Ser Ala Ile Gly

435 440 445

Arg Ala Met Glu Leu Gln Lys Ala Arg His Pro Lys His Leu Ser Thr
450 455 460

Pro Ser Ser Val Ser Pro Glu Pro Gln Asp Ser Ala Lys Leu Arg Gln
465 470 475 480

Ser Gly Leu Ala Asn Glu Gly Thr Asp Ala Gly Tyr Leu Pro Ala Asn
485 490 495

Ser Met Ser Ser Val Ala Ser Gly Ala Ser Phe Ser Gln Glu Gly Gly
500 505 510

Lys Glu Asn Asp Thr Gly Ser Lys Gln Val Gly Glu Thr Ser Ala Pro
515 520 525

Gly Asp Thr Leu Asp Gly Thr Pro Arg Thr Leu Asn Thr Val Phe Asp
530 535 540

Phe Pro Pro Pro Pro Leu Asp Gln Val Gln Glu Glu Glu Cys Glu Val
545 550 555 560

Glu Arg Val Thr Glu His Gly Thr Pro Lys Pro Phe Arg Lys Phe Asp
565 570 575

Ser Val Ala Phe Gly Glu Ser Gln Ser Glu Asp Glu Gln Phe Glu Asn
580 585 590

Asp Leu Glu Thr Asp Pro Pro Asn Trp Gln Gln Leu Val Ser Arg Glu
595 600 605

Val Leu Leu Gly Leu Lys Pro Cys Glu Ile Lys Arg Gln Glu Val Ile
610 615 620

Asn Glu Leu Phe Tyr Thr Glu Arg Ala His Val Arg Thr Leu Lys Val
625 630 635 640

Leu Asp Gln Val Phe Tyr Gln Arg Val Ser Arg Glu Gly Ile Leu Ser
645 650 655

Pro Ser Glu Leu Arg Lys Ile Phe Ser Asn Leu Glu Asp Ile Leu Gln
660 665 670

Leu His Ile Gly Leu Asn Glu Gln Met Lys Ala Val Arg Lys Arg Asn
675 680 685

Glu Thr Ser Val Ile Asp Gln Ile Gly Glu Asp Leu Leu Thr Trp Phe
690 695 700

Ser Gly Pro Gly Glu Glu Lys Leu Lys His Ala Ala Ala Thr Phe Cys
705 710 715 720

Ser Asn Gln Pro Phe Ala Leu Glu Met Ile Lys Ser Arg Gln Lys Lys
725 730 735

Asp Ser Arg Phe Gln Thr Phe Val Gln Asp Ala Glu Ser Asn Pro Leu
740 745 750

Cys Arg Arg Leu Gln Leu Lys Asp Ile Ile Pro Thr Gln Met Gln Arg

755 760 765

Leu Thr Lys Tyr Pro Leu Leu Leu Asp Asn Ile Ala Lys Tyr Thr Glu
770 775 780

Trp Pro Thr Glu Arg Glu Lys Val Lys Lys Ala Ala Asp His Cys Arg
785 790 795 800

Gln Ile Leu Asn Tyr Val Asn Gln Ala Val Lys Glu Ala Glu Asn Lys
805 810 815

Gln Arg Leu Glu Asp Tyr Gln Arg Arg Leu Asp Thr Ser Ser Leu Lys
820 825 830

Leu Ser Glu Tyr Pro Asn Val Glu Glu Leu Arg Asn Leu Asp Leu Thr
835 840 845

Lys Arg Lys Met Ile His Glu Gly Pro Leu Val Trp Lys Val Asn Arg
850 855 860

Asp Lys Thr Ile Asp Leu Tyr Thr Leu Leu Leu Glu Asp Ile Leu Val
865 870 875 880

Leu Leu Gln Lys Gln Asp Asp Arg Leu Val Leu Arg Cys His Ser Lys
885 890 895

Ile Leu Ala Ser Thr Ala Asp Ser Lys His Thr Phe Ser Pro Val Ile
900 905 910

Lys Leu Ser Thr Val Leu Val Arg Gln Val Ala Thr Asp Asn Lys Ala
915 920 925

Leu Phe Val Ile Ser Met Ser Asp Asn Gly Ala Gln Ile Tyr Glu Leu
930 935 940

Val Ala Gln Thr Val Ser Glu Lys Thr Val Trp Gln Asp Leu Ile Cys
945 950 955 960

Arg Met Ala Ala Ser Val Lys Glu Gln Ser Thr Lys Pro Ile Pro Leu
965 970 975

Pro Gln Ser Thr Pro Gly Glu Gly Asp Asn Asp Glu Glu Asp Pro Ser
980 985 990

Lys Leu Lys Glu Glu Gln His Gly Ile Ser Val Thr Gly Leu Gln Ser
995 1000 1005

Pro Asp Arg Asp Leu Gly Leu Glu Ser Thr Leu Ile Ser Ser Lys Pro
1010 1015 1020

Gln Ser His Ser Leu Ser Thr Ser Gly Lys Ser Glu Val Arg Asp Leu
1025 1030 1035 1040

Phe Val Ala Glu Arg Gln Phe Ala Lys Glu Gln His Thr Asp Gly Thr
1045 1050 1055

Leu Lys Glu Val Gly Glu Asp Tyr Gln Ile Ala Ile Pro Asp Ser His
1060 1065 1070

Leu Pro Val Ser Glu Glu Arg Trp Ala Leu Asp Ala Leu Arg Asn Leu

1075 1080 1085

Gly Leu Leu Lys Gln Leu Leu Val Gln Gln Leu Gly Leu Thr Glu Lys
1090 1095 1100

Ser Val Gln Glu Asp Trp Gln His Phe Pro Arg Tyr Arg Thr Ala Ser
1105 1110 1115 1120

Gln Gly Pro Gln Thr Asp Ser Val Ile Gln Asn Ser Glu Asn Ile Lys
1125 1130 1135

Ala Tyr His Ser Gly Glu Gly His Met Pro Phe Arg Thr Gly Thr Gly
1140 1145 1150

Asp Ile Ala Thr Cys Tyr Ser Pro Arg Thr Ser Thr Glu Ser Phe Ala
1155 1160 1165

Pro Arg Asp Ser Val Gly Leu Ala Pro Gln Asp Ser Gln Ala Ser Asn
1170 1175 1180

Ile Leu Val Met Asp His Met Ile Met Thr Pro Glu Met Pro Thr Met
1185 1190 1195 1200

Glu Pro Glu Gly Gly Leu Asp Asp Ser Gly Glu His Phe Phe Asp Ala
1205 1210 1215

Arg Glu Ala His Ser Asp Glu Asn Pro Ser Glu Gly Asp Gly Ala Val
1220 1225 1230

Asn Lys Glu Glu Lys Asp Val Asn Leu Arg Ile Ser Gly Asn Tyr Leu
1235 1240 1245

Ile Leu Asp Gly Tyr Asp Pro Val Gln Glu Ser Ser Thr Asp Glu Glu
1250 1255 1260

Val Ala Ser Ser Leu Thr Leu Gln Pro Met Thr Gly Ile Pro Ala Val
1265 1270 1275 1280

Glu Ser Thr His Gln Gln Gln His Ser Pro Gln Asn Thr His Ser Asp
1285 1290 1295

Gly Ala Ile Ser Pro Phe Thr Pro Glu Phe Leu Val Gln Gln Arg Trp
1300 1305 1310

Gly Ala Met Glu Tyr Ser Cys Phe Glu Ile Gln Ser Pro Ser Ser Cys
1315 1320 1325

Ala Asp Ser Gln Ser Gln Ile Met Glu Tyr Ile His Lys Ile Glu Ala
1330 1335 1340

Asp Leu Glu His Leu Lys Glu Gly Gly Gly Lys Leu Thr Pro Phe Phe
1345 1350 1355 1360

Ala Lys Gly Trp Leu Asp Gln Pro Ser Gln Thr Ser Thr Gln Ile Lys
1365 1370 1375

Val Arg Ala Ala Cys Pro Gly Gly Asp Cys Arg Leu Leu Asp Leu Glu
1380 1385 1390

Tyr Arg Pro Cys Leu Thr Thr Ser Trp Leu Gln Cys Gly Cys Arg Glu

1395 1400 1405

Ser Val Thr Glu Asp Leu Pro Val Asn His Leu Gly Leu Val Lys Ser
1410 1415 1420

Gln Gly Ala Gln Ser Gly Thr Ser Xaa Ser Gln Cys Gly Ser Cys Thr
1425 1430 1435 1440

Asn Leu Phe Val Arg Glu Tyr Pro Phe Pro His Ser Thr Leu Leu Thr
1445 1450 1455

Ile Gly Asn Ser Phe
1460

<210> 187
<211> 2837
<212> DNA
<213> Homo sapiens

<400> 187
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gggagagaaa aaagaatcaa agccagctgc taccacacgc tcttctggag gaggaggtgg 180
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gggtgacatt ccatgggacg acaaggattt caggatgttc ttcctctgga ctgctctgtt 300
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aaccactgcc aaggtcttaa aggatgaaat tgatgtgaag ttcaaagatg tggctggctg 780
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<210> 188
<211> 686
<212> PRT
<213> Homo sapiens

<400> 188
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Gly Gly Gly Gly Gly Gly Gly Gly Lys Arg Gly Gly Lys Lys Asp Asp
20 25 30

Ser His Trp Trp Ser Arg Phe Gln Lys Gly Asp Ile Pro Trp Asp Asp
35 40 45

Lys Asp Phe Arg Met Phe Phe Leu Trp Thr Ala Leu Phe Trp Gly Gly
50 55 60

Val Met Phe Tyr Leu Leu Leu Lys Arg Ser Gly Arg Glu Ile Thr Trp
65 70 75 80

Lys Asp Phe Val Asn Asn Tyr Leu Ser Lys Gly Val Val Asp Arg Leu
85 90 95

Glu Val Val Asn Lys Arg Phe Val Arg Val Thr Phe Thr Pro Gly Lys
100 105 110

Thr Pro Val Asp Gly Gln Tyr Val Trp Phe Asn Ile Gly Ser Val Asp
115 120 125

Thr Phe Glu Arg Asn Leu Glu Thr Leu Gln Gln Glu Leu Gly Ile Glu
130 135 140

Gly Glu Asn Arg Val Pro Val Val Tyr Ile Ala Glu Ser Asp Gly Ser
145 150 155 160

Phe Leu Leu Ser Met Leu Pro Thr Val Leu Ile Ile Ala Phe Leu Leu
165 170 175

Tyr Thr Ile Arg Arg Gly Pro Ala Gly Ile Gly Arg Thr Gly Arg Gly
180 185 190

Met Gly Gly Leu Phe Ser Val Gly Glu Thr Thr Ala Lys Val Leu Lys
195 200 205

Asp Glu Ile Asp Val Lys Phe Lys Asp Val Ala Gly Cys Glu Glu Ala
210 215 220

Lys Leu Glu Ile Met Glu Phe Val Asn Phe Leu Lys Asn Pro Lys Gln
225 230 235 240

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Tyr Gln Asp Leu Gly Ala Ile Ile Pro Lys Gly Ala Ile Leu Thr Gly
                245                 250                 255

Pro Pro Gly Thr Gly Lys Thr Leu Leu Ala Lys Ala Thr Ala Gly Glu
            260                 265                 270

Ala Asn Val Pro Phe Ile Thr Val Ser Gly Ser Glu Phe Leu Glu Met
        275                 280                 285

Phe Val Gly Val Gly Pro Ala Arg Val Arg Asp Leu Phe Ala Leu Ala
    290                 295                 300

Arg Lys Asn Ala Pro Cys Ile Leu Phe Ile Asp Glu Ile Asp Ala Val
305                 310                 315                 320

Gly Arg Lys Arg Gly Arg Gly Asn Phe Gly Gly Gln Ser Glu Gln Glu
                325                 330                 335

Asn Thr Leu Asn Gln Leu Leu Val Glu Met Asp Gly Phe Asn Thr Thr
            340                 345                 350

Thr Asn Val Val Ile Leu Ala Gly Thr Asn Arg Pro Gly Pro Pro Asp
        355                 360                 365

Ile Lys Gly Arg Ala Ser Ile Phe Lys Val His Leu Arg Pro Leu Lys
    370                 375                 380

Leu Asp Ser Thr Leu Glu Lys Asp Lys Leu Ala Arg Lys Leu Ala Ser
385                 390                 395                 400

Leu Thr Pro Gly Phe Ser Gly Ala Asp Val Ala Asn Val Cys Asn Glu
                405                 410                 415

Ala Ala Leu Ile Ala Ala Arg His Leu Ser Asp Ser Ile Asn Gln Lys
            420                 425                 430

His Phe Glu Gln Ala Ile Glu Arg Val Ile Gly Gly Leu Lys Lys Lys
        435                 440                 445

Thr Gln Val Leu Gln Pro Glu Glu Lys Lys Thr Val Ala Tyr His Glu
    450                 455                 460

Ala Gly His Ala Val Ala Gly Trp Tyr Leu Glu His Ala Asp Pro Leu
465                 470                 475                 480

Leu Lys Val Ser Ile Ile Pro Arg Gly Lys Gly Leu Gly Tyr Ala Gln
                485                 490                 495

Tyr Leu Pro Lys Glu Gln Tyr Leu Tyr Thr Lys Glu Gln Leu Leu Asp
            500                 505                 510

Arg Met Cys Met Thr Leu Gly Gly Arg Val Ser Glu Glu Ile Phe Phe
        515                 520                 525

Gly Arg Ile Thr Thr Gly Ala Gln Asp Asp Leu Arg Lys Val Thr Gln
    530                 535                 540

Ser Ala Tyr Ala Gln Ile Val Gln Phe Gly Met Asn Glu Lys Val Gly
545                 550                 555                 560
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Gln Ile Ser Phe Asp Leu Pro Arg Gln Gly Asp Met Val Leu Glu Lys
565 570 575

Pro Tyr Ser Glu Ala Thr Ala Arg Leu Ile Asp Asp Glu Val Arg Ile
580 585 590

Leu Ile Asn Asp Ala Tyr Lys Arg Thr Val Ala Leu Leu Thr Glu Lys
595 600 605

Lys Ala Asp Val Glu Lys Val Ala Leu Leu Leu Leu Glu Lys Glu Val
610 615 620

Leu Asp Lys Asn Asp Met Val Glu Leu Leu Gly Pro Arg Pro Phe Ala
625 630 635 640

Glu Lys Ser Thr Tyr Glu Glu Phe Val Glu Gly Thr Gly Ser Leu Asp
645 650 655

Glu Asp Thr Ser Leu Pro Glu Gly Leu Lys Asp Trp Asn Lys Glu Arg
660 665 670

Glu Lys Glu Lys Glu Glu Pro Pro Gly Glu Lys Val Ala Asn
675 680 685

<210> 189
<211> 627
<212> DNA
<213> Homo sapiens

<400> 189
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aaagttgatt aactatttcg tgtgctaatt tgagtttttc tgaatactcc aatatggttt 180
cctttaacac ctgctctcag tttacaatca cctaacttcc cagcgttggt gtctttttct 240
ctgtctgacc ctgtcttatt tctcctacaa agacatatcc tgcgctgtac ttcagatact 300
tttttcgagg aacatttgtg atttgtggca taaagtaact gtctaaagga aatcttctga 360
gaggatctgg tcattttatg aaaggggcaa ttaaggggaa atggaagcag atcttttaaa 420
gaaggagcat ttgaaattag cccaggaatc atgtccggcg agtcctgctc ttttgtacct 480
gggcataata gtcagccaca cagagctaga gttagttcaa gaattgtctt tcctgatcgt 540
gctatatttt tggaaacacg ttagatacag aggtaagatg tcaaaattct gaaatacaca 600
caatatagga tcaaaaaaaa aaaaaaa 627

<210> 190
<211> 63
<212> PRT
<213> Homo sapiens

<400> 190
Met Glu Ala Asp Leu Leu Lys Lys Glu His Leu Lys Leu Ala Gln Glu
1 5 10 15

Ser Cys Pro Ala Ser Pro Ala Leu Leu Tyr Leu Gly Ile Ile Val Ser
20 25 30

His Thr Glu Leu Glu Leu Val Gln Glu Leu Ser Phe Leu Ile Val Leu
35 40 45

Tyr Phe Trp Lys His Val Arg Tyr Arg Gly Lys Met Ser Lys Phe

50 55 60

<210> 191
<211> 868
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (733)

<400> 191
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ctggctccat tggcttctcc ctgcaccagc cctgtcctca ggggtcagga aaaagcacac 180
agctttcttt cctctcctcc agaggcctgg aagggaggtg gaggtccagt aagggcctgg 240
ctgccttgga tttcttggtc ctgccttgcc aactgcaccc tgtagctcct gctccctgtg 300
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aggacagatg ctagttgtag tttcactcac tcattcattc attagtgcaa cagtactgag 600
caccacctgc actagaggca gaggggtgaa caagataccc ttttgcctgg ggggacgtcc 660
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cccaagcact ggcagctttg cagcccct 868

<210> 192
<211> 107
<212> PRT
<213> Homo sapiens

<220>
<221> UNSURE
<222> (62)

<400> 192
Met Leu Val Val Val Ser Leu Thr His Ser Phe Ile Ser Ala Thr Val
1 5 10 15

Leu Ser Thr Thr Cys Thr Arg Gly Arg Gly Val Asn Lys Ile Pro Phe
20 25 30

Cys Leu Gly Gly Arg Pro Leu Pro Met Gly Leu Ala Ile Ser Arg Lys
35 40 45

Ala Pro Gln Ser Ser Ser Leu Phe Trp Leu Cys Val Lys Xaa Val Cys
50 55 60

Glu Gln Ala Gln Ser Phe Ala Ala Arg Met Arg Gly Gln Ser Ile Pro
65 70 75 80

Leu His Thr His Pro Gly Ala Asp Arg Leu Val Pro Pro Ser Leu His
85 90 95

Ala Cys Pro Ser Thr Gly Ser Phe Ala Ala Pro
100 105

<210> 193
<211> 467
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (57)

<220>
<221> unsure
<222> (254)

<400> 193
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cccaggtatg tgtagaggcc cagtgggggt ggccacttgg tgtttctacc accccctgcc 180
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gagccagccc ctcaggaatt gcctcaaaag agaaaaaaaa aaaaaaa 467

<210> 194
<211> 1035
<212> DNA
<213> Homo sapiens

<400> 194
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acttcgaatt cggccttcat ggcctagatg attgcaagtc aatggaagga gctgcagagg 180
caaatcaaac ggcagcacag ctggattctc agggctctgg ataccatcaa agccgagata 240
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<210> 195
<211> 179
<212> PRT
<213> Homo sapiens

<220>
<221> UNSURE
<222> (37)

<220>
<221> UNSURE

<222> (73)

<400> 195

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Phe Asn Tyr Ala Thr Trp Lys His Lys Glu Met Leu Leu Ser Arg Cys
            20                  25                  30

Pro Ser Ser Cys Xaa Ala Ser Ser Ile Pro Ala Ala Ala Ser Glu Arg
        35                  40                  45

Lys Ser Leu Leu Ile Cys Gln Lys Phe His Ser Val Gly Ser Asn Gly
    50                  55                  60

Leu Leu Asp Phe Asp Ser Glu Tyr Xaa Glu Leu Trp Asp Trp Leu Ile
65                  70                  75                  80

Asp Met Glu Ser Leu Val Met Asp Ser His Asp Leu Met Met Ser Glu
                85                  90                  95

Glu Gln Gln Gln His Leu Tyr Lys Arg Tyr Ser Val Glu Met Ser Ile
            100                 105                 110

Arg His Leu Lys Lys Thr Glu Leu Leu Ser Lys Val Glu Ala Leu Lys
        115                 120                 125

Lys Gly Gly Val Leu Leu Pro Asn Asp Leu Leu Glu Lys Val Asp Ser
    130                 135                 140

Ile Asn Glu Lys Trp Glu Leu Leu Gly Val Phe Ala Phe Leu Leu Leu
145                 150                 155                 160

Phe Val Gly Tyr Val Tyr Ile Phe Cys Val Val Lys Tyr Ser Val Arg
                165                 170                 175

Phe Leu Ile
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<210> 196
<211> 3831
<212> DNA
<213> Homo sapiens

<400> 196

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atgttaacca tgagcgtgac actttccccc ctgaggtcac aggacctgga tcccatggct 180
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cacaaaagca aaaaaggtca agcctcctct ccaagtcacg tcactaggaa tggtgaggtt 1980
gtggaggcct ggtatggctc tgatgaatac ctagcactgc cctctcacct taagcagaca 2040
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caaaacaaag atgcaaattt gacccaaatc tgaattgcag aattgaatca gcctgtgttt 3780
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<210> 197
<211> 1075
<212> PRT
<213> Homo sapiens

<400> 197
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1 5 10 15

Asp Pro Met Ala Thr Asp Ala Ser Pro Met Ala Ile Asn Met Thr Pro
20 25 30

Thr Val Glu Gln Gly Glu Gly Glu Glu Ala Met Lys Asp Met Asp Ser
35 40 45

Asp Gln Gln Tyr Glu Lys Pro Pro Pro Leu His Thr Gly Ala Asp Trp
50 55 60

Lys Ile Val Leu His Leu Pro Glu Ile Glu Thr Trp Leu Arg Met Thr
65 70 75 80

Ser Glu Arg Val Arg Asp Leu Thr Tyr Ser Val Gln Gln Asp Ser Asp
85 90 95

Ser Lys His Val Asp Val His Leu Val Gln Leu Lys Asp Ile Cys Glu
100 105 110

Asp Ile Ser Asp His Val Glu Gln Ile His Ala Leu Leu Glu Thr Glu
115 120 125

Phe Ser Leu Lys Leu Leu Ser Tyr Ser Val Asn Val Ile Val Asp Ile
130 135 140

His Ala Val Gln Leu Leu Trp His Gln Leu Arg Val Ser Val Leu Val
145 150 155 160

Leu Arg Glu Arg Ile Leu Gln Gly Leu Gln Asp Ala Asn Gly Asn Tyr
165 170 175

Thr Arg Gln Thr Asp Ile Leu Gln Ala Phe Ser Glu Glu Thr Lys Glu
180 185 190

Gly Arg Leu Asp Ser Leu Thr Glu Val Asp Asp Ser Gly Gln Leu Thr
195 200 205

Ile Lys Cys Ser Gln Asn Tyr Leu Ser Leu Asp Cys Gly Ile Thr Ala
210 215 220

Phe Glu Leu Ser Asp Tyr Ser Pro Ser Glu Asp Leu Leu Ser Gly Leu
225 230 235 240

Gly Asp Met Thr Ser Ser Gln Val Lys Thr Lys Pro Phe Asp Ser Trp
245 250 255

Ser Tyr Ser Glu Met Glu Lys Glu Phe Pro Glu Leu Ile Arg Ser Val
260 265 270

Gly Leu Leu Thr Val Ala Ala Asp Ser Ile Ser Thr Asn Gly Ser Glu
275 280 285

Ala Val Thr Glu Glu Val Ser Gln Val Ser Leu Ser Val Asp Asp Lys
290 295 300

Gly Gly Cys Glu Glu Asp Asn Ala Ser Ala Val Glu Glu Gln Pro Gly
305 310 315 320

Leu Thr Leu Gly Val Ser Ser Ser Ser Gly Glu Ala Leu Thr Asn Ala
325 330 335

Ala Gln Pro Ser Ser Glu Thr Val Gln Gln Glu Ser Ser Ser Ser Ser
340 345 350

His His Asp Ala Lys Asn Gln Gln Pro Val Pro Cys Glu Asn Ala Thr
355 360 365

Pro Lys Arg Thr Ile Arg Asp Cys Phe Asn Tyr Asn Glu Asp Ser Pro
370 375 380

Thr Gln Pro Thr Leu Pro Lys Arg Gly Leu Phe Leu Lys Glu Glu Thr
385 390 395 400

Phe Lys Asn Asp Leu Lys Gly Asn Gly Gly Lys Arg Gln Met Val Asp
405 410 415

Leu Lys Pro Glu Met Ser Arg Ser Thr Pro Ser Leu Val Asp Pro Pro
420 425 430

Asp Arg Ser Lys Leu Cys Leu Val Leu Gln Ser Ser Tyr Pro Asn Ser
435 440 445

Pro Ser Ala Ala Ser Gln Ser Tyr Glu Cys Leu His Lys Val Gly Asn
450 455 460

Gly Asn Leu Glu Asn Thr Val Lys Phe His Ile Lys Glu Ile Ser Ser
465 470 475 480

Ser Leu Gly Arg Leu Asn Asp Cys Tyr Lys Glu Lys Ser Arg Leu Lys
485 490 495

Lys Pro His Lys Thr Ser Glu Glu Val Pro Pro Cys Arg Thr Pro Lys
500 505 510

Arg Gly Thr Gly Ser Gly Lys Gln Ala Lys Asn Thr Lys Ser Ser Ala
515 520 525

Val Pro Asn Gly Glu Leu Ser Tyr Thr Ser Lys Ala Ile Glu Gly Pro
530 535 540

Gln Thr Asn Ser Ala Ser Thr Ser Ser Leu Glu Pro Cys Asn Gln Arg
545 550 555 560

Ser Trp Asn Ala Lys Leu Gln Leu Gln Ser Glu Thr Ser Ser Ser Pro
565 570 575

Ala Phe Thr Gln Ser Ser Glu Ser Ser Val Gly Ser Asp Asn Ile Met
580 585 590

Ser Pro Val Pro Leu Leu Ser Lys His Lys Ser Lys Lys Gly Gln Ala
595 600 605

Ser Ser Pro Ser His Val Thr Arg Asn Gly Glu Val Val Glu Ala Trp
610 615 620

Tyr Gly Ser Asp Glu Tyr Leu Ala Leu Pro Ser His Leu Lys Gln Thr
625 630 635 640

Glu Val Leu Ala Leu Lys Leu Glu Asn Leu Thr Lys Leu Leu Pro Gln
645 650 655

Lys Pro Arg Gly Glu Thr Ile Gln Asn Ile Asp Asp Trp Glu Leu Ser
660 665 670

Glu Met Asn Ser Asp Ser Glu Ile Tyr Pro Thr Tyr His Val Lys Lys
675 680 685

Lys His Thr Arg Leu Gly Arg Val Ser Pro Ser Ser Ser Ser Asp Ile
690 695 700

Ala Ser Ser Leu Gly Glu Ser Ile Glu Ser Gly Pro Leu Ser Asp Ile
705 710 715 720

Leu Ser Asp Glu Glu Ser Ser Met Pro Leu Ala Gly Met Lys Lys Tyr
725 730 735

Ala Asp Glu Lys Ser Glu Arg Ala Ser Ser Ser Glu Lys Asn Glu Ser
740 745 750

His Ser Ala Thr Lys Ser Ala Leu Ile Gln Lys Leu Met Gln Asp Ile
755 760 765

Gln His Gln Asp Asn Tyr Glu Ala Ile Trp Glu Lys Ile Glu Gly Phe
770 775 780

Val Asn Lys Leu Asp Glu Phe Ile Gln Trp Leu Asn Glu Ala Met Glu
785 790 795 800

Thr Thr Glu Asn Trp Thr Pro Pro Lys Ala Glu Met Asp Asp Leu Lys
805 810 815

Leu Tyr Leu Glu Thr His Leu Ser Phe Lys Leu Asn Val Asp Ser His
820 825 830

Cys Ala Leu Lys Glu Ala Val Glu Glu Glu Gly His Gln Leu Leu Glu
835 840 845

Leu Ile Ala Ser His Lys Ala Gly Leu Lys Asp Met Leu Arg Met Ile
850 855 860

Ala Ser Gln Trp Lys Glu Leu Gln Arg Gln Ile Lys Arg Gln His Ser
865 870 875 880

Trp Ile Leu Arg Ala Leu Asp Thr Ile Lys Ala Glu Ile Leu Ala Thr
885 890 895

Asp Val Ser Val Glu Asp Glu Glu Gly Thr Gly Ser Pro Lys Ala Glu
900 905 910

Val Gln Leu Cys Tyr Leu Glu Ala Gln Arg Asp Ala Val Glu Gln Met
915 920 925

Ser Leu Lys Leu Tyr Ser Glu Gln Tyr Thr Ser Ser Ser Lys Arg Lys
930 935 940

Glu Glu Phe Ala Asp Met Ser Lys Val His Ser Val Gly Ser Asn Gly
945 950 955 960

Leu Leu Asp Phe Asp Ser Glu Tyr Gln Glu Leu Trp Asp Trp Leu Ile
965 970 975

Asp Met Glu Ser Leu Val Met Asp Ser His Asp Leu Met Met Ser Glu
980 985 990

Glu Gln Gln Gln His Leu Tyr Lys Arg Tyr Ser Val Glu Met Ser Ile
995 1000 1005

Arg His Leu Lys Lys Thr Glu Leu Leu Ser Lys Val Glu Ala Leu Lys
1010 1015 1020

Lys Gly Gly Val Leu Leu Pro Asn Asp Leu Leu Glu Lys Val Asp Ser
1025 1030 1035 1040

Ile Asn Glu Lys Trp Glu Leu Leu Gly Val Phe Ala Phe Leu Leu Leu
1045 1050 1055

Phe Val Gly Tyr Val Tyr Ile Phe Cys Val Val Lys Tyr Ser Val Arg
1060 1065 1070

Phe Leu Ile
1075

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<211> 3113
<212> DNA
<213> Homo sapiens

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acaaagatct cagtggatat aaaggttcaa gcactcccac caaaggcata gagaacaaag 180
cttttgatcg caatacagaa tctctctttg aagaactgtc ttcagctggc tcaggcctaa 240
taggagatgt ggatgaagga gcagatttac taggaatggg tcgggaagtt gagaatctta 300
tattagaaaa tacacaactg ttggaaacca aaaatgcttt gaacatagtg aagaatgatt 360
tgatagcaaa agtggatgaa ctgacctgtg agaaagatgt gctgcaaggg gaattggagg 420
ctgtgaagca agccaaactg aaactagagg aaaagaacag agaattggag gaagagctta 480
ggaaagctcg ggcagaagct gaagatgcag ggcaaaaagc aaaagatgac gatgatagtg 540
atattcccac agcccagagg aaacggttta ctagagtaga aatggcccgt gttctcatgg 600
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tgattcgggc atcacgagaa aatccagcca tgcaggaaaa aaaaaggtca agcatttggc 720
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gcaccttatc tcagctccct ggggataagt ccaaagcctt tgatttcctt agtgaagaaa 900
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aacaagactt ggtgagagaa gaagcccaga aaatgagtag tcttttacca actatgtggc 1980
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<211> 828
<212> PRT
<213> Homo sapiens

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Gly Ile Glu Asn Lys Ala Phe Asp Arg Asn Thr Glu Ser Leu Phe Glu
20 25 30

Glu Leu Ser Ser Ala Gly Ser Gly Leu Ile Gly Asp Val Asp Glu Gly
35 40 45

Ala Asp Leu Leu Gly Met Gly Arg Glu Val Glu Asn Leu Ile Leu Glu
50 55 60

Asn Thr Gln Leu Leu Glu Thr Lys Asn Ala Leu Asn Ile Val Lys Asn
65 70 75 80

Asp Leu Ile Ala Lys Val Asp Glu Leu Thr Cys Glu Lys Asp Val Leu
85 90 95

Gln Gly Glu Leu Glu Ala Val Lys Gln Ala Lys Leu Lys Leu Glu Glu
100 105 110

Lys Asn Arg Glu Leu Glu Glu Glu Leu Arg Lys Ala Arg Ala Glu Ala
115 120 125

Glu Asp Ala Gly Gln Lys Ala Lys Asp Asp Asp Asp Ser Asp Ile Pro
130 135 140

Thr Ala Gln Arg Lys Arg Phe Thr Arg Val Glu Met Ala Arg Val Leu
145 150 155 160

Met Glu Arg Asn Gln Tyr Lys Glu Arg Leu Met Glu Leu Gln Glu Ala
165 170 175

Val Arg Trp Thr Glu Met Ile Arg Ala Ser Arg Glu Asn Pro Ala Met
180 185 190

Gln Glu Lys Lys Arg Ser Ser Ile Trp Gln Phe Phe Ser Arg Leu Phe
195 200 205

Ser Ser Ser Ser Asn Thr Thr Lys Lys Pro Glu Pro Pro Val Asn Leu
210 215 220

Lys Tyr Asn Ala Pro Thr Ser His Val Thr Pro Ser Val Lys Lys Arg
225 230 235 240

Ser Ser Thr Leu Ser Gln Leu Pro Gly Asp Lys Ser Lys Ala Phe Asp
245 250 255

Phe Leu Ser Glu Glu Thr Glu Ala Ser Leu Ala Ser Arg Arg Glu Gln
260 265 270

Lys Arg Glu Gln Tyr Arg Gln Val Lys Ala His Val Gln Lys Glu Asp
275 280 285

Gly Arg Val Gln Ala Phe Gly Trp Ser Leu Pro Gln Lys Tyr Lys Gln
290 295 300

Val Thr Asn Gly Gln Gly Glu Asn Lys Met Lys Asn Leu Pro Val Pro
305 310 315 320

Val Tyr Leu Arg Pro Leu Asp Glu Lys Asp Thr Ser Met Lys Leu Trp
325 330 335

Cys Ala Val Gly Val Asn Leu Ser Gly Gly Lys Thr Arg Asp Gly Gly
340 345 350

Ser Val Val Gly Ala Ser Val Phe Tyr Lys Asp Val Ala Gly Leu Asp
355 360 365

Thr Glu Gly Ser Lys Gln Arg Ser Ala Ser Gln Ser Ser Leu Asp Lys
370 375 380

Leu Asp Gln Glu Leu Lys Glu Gln Gln Lys Glu Leu Lys Asn Gln Glu
385 390 395 400

Glu Leu Ser Ser Leu Val Trp Ile Cys Thr Ser Thr His Ser Ala Thr
405 410 415

Lys Val Leu Ile Ile Asp Ala Val Gln Pro Gly Asn Ile Leu Asp Ser
420 425 430

Phe Thr Val Cys Asn Ser His Val Leu Cys Ile Ala Ser Val Pro Gly
435 440 445

Ala Arg Glu Thr Asp Tyr Pro Ala Gly Glu Asp Leu Ser Glu Ser Gly
450 455 460

Gln Val Asp Lys Ala Ser Leu Cys Gly Ser Met Thr Ser Asn Ser Ser
465 470 475 480

Ala Glu Thr Asp Ser Leu Leu Gly Gly Ile Thr Val Val Gly Cys Ser
485 490 495

Ala Glu Gly Val Thr Gly Ala Ala Thr Ser Pro Ser Thr Asn Gly Ala
500 505 510

Ser Pro Val Met Asp Lys Pro Pro Glu Met Glu Ala Glu Asn Ser Glu
515 520 525

Val Asp Glu Asn Val Pro Thr Ala Glu Glu Ala Thr Glu Ala Thr Glu
530 535 540

Gly Asn Ala Gly Ser Ala Glu Asp Thr Val Asp Ile Ser Gln Thr Gly
545 550 555 560

Val Tyr Thr Glu His Val Phe Thr Asp Pro Leu Gly Val Gln Ile Pro
565 570 575

Glu Asp Leu Ser Pro Val Tyr Gln Ser Ser Asn Asp Ser Asp Ala Tyr
580 585 590

Lys Asp Gln Ile Ser Val Leu Pro Asn Glu Gln Asp Leu Val Arg Glu
595 600 605

Glu Ala Gln Lys Met Ser Ser Leu Leu Pro Thr Met Trp Leu Gly Ala
610 615 620

Gln Asn Gly Cys Leu Tyr Val His Ser Ser Val Ala Gln Trp Arg Lys
625 630 635 640

Cys Leu His Ser Ile Lys Leu Lys Asp Ser Ile Leu Ser Ile Val His
645 650 655

Val Lys Gly Ile Val Leu Val Ala Leu Ala Asp Gly Thr Leu Ala Ile
660 665 670

Phe His Arg Gly Val Asp Gly Gln Trp Asp Leu Ser Asn Tyr His Leu
675 680 685

Leu Asp Leu Gly Arg Pro His His Ser Ile Arg Cys Met Thr Val Val
690 695 700

His Asp Lys Val Trp Cys Gly Tyr Arg Asn Lys Ile Tyr Val Val Gln
705 710 715 720

Pro Lys Ala Met Lys Ile Glu Lys Ser Phe Asp Ala His Pro Arg Lys
725 730 735

Glu Ser Gln Val Arg Gln Leu Ala Trp Val Gly Asp Gly Val Trp Val
740 745 750

Ser Ile Arg Leu Asp Ser Thr Leu Arg Leu Tyr His Ala His Thr Tyr
755 760 765

Gln His Leu Gln Asp Val Asp Ile Glu Pro Tyr Val Ser Lys Met Leu
770 775 780

Gly Thr Gly Lys Leu Gly Phe Ser Phe Val Arg Ile Thr Ala Leu Met
785 790 795 800

Val Ser Cys Asn Arg Leu Trp Val Gly Thr Gly Asn Gly Val Ile Ile
805 810 815

Ser Ile Pro Leu Thr Glu Ser Lys Tyr Ile Phe Arg
820 825

<210> 200
<211> 29
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<213> Artificial Sequence

<220>
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<220>
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<222> (2)
<223> biotinylated phosphoaramidite residue

<400> 200
tnaggtttgc acttcttctt gcaaattcc 29

<210> 201
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<220>
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<222> (2)
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<400> 201
cnaatatctg agtctgtcct gcgggactc 29

<210> 202
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
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<400> 202
cnggctctgt gatggctgaa tggaaagaa 29

<210> 203
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
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<400> 203
angagtccaa ttaaagaacg aaaagcggg 29

<210> 204
<211> 29
<212> DNA
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<220>
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<400> 204
cntcagcttg ggcaagagta aagagggca 29

<210> 205
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<400> 205
tnatttaaga tgctgtgtaa gcctctcgc 29

<210> 206
<211> 29
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<220>
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tntctgtgtg cacagagctt tggagtggc 29

<210> 207
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<220>
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<400> 207
gnttggattc tctggcagag tacacctgc 29

<210> 208
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<220>
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<222> (2)
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<400> 208
gnaggcatat cttttacagg ttcagctcc 29

<210> 209
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
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<220>
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<400> 209
cncagtgaga caggtagtag gagccagat 29

<210> 210
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<220>
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<400> 210
angtaaattc cagccaggat gatggccgc 29

<210> 211
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<220>
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<400> 211
tngagtgtgg aattgcgctt cttacctat 29

<210> 212
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<400> 212
gngtgaagtc ttcctgggaa ccataatct 29

<210> 213
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<400> 213
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<210> 216
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<400> 216
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<210> 217
<211> 29
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20 25 30

Lys Ala Gly Ala Thr Pro Ser Ser Leu Phe Ser Thr Gln His Gln Ala

35 40 45

Leu Ser Arg His Pro Ile Asn His Cys
50 55

Applicant's or agent's file reference 1290.1001010	International application No. PCT/US 00/ 25135

INDICATIONS RELATING TO DEPOSITED MICROORGANISM OR OTHER BIOLOGICAL MATERIAL

(PCT Rule 13*bis*)

A. The indications made below relate to the deposited microorganism or other biological material referred to in the description on pages 333 335, line 32 to 35

B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet ☐

Name of depositary institution

AMERICAN TYPE CULTURE COLLECTION

Address of depositary institution *(including postal code and country)*

American Type Culture Collection (ATCC)
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

Date of deposit	Accession Number
see Attachment A	see Attachment A

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* This information is continued on an additional sheet ☒

In respect of those designations for which a European patent is sought, the Applicant(s) hereby informs the International Bureau that the Applicant wishes that, until the publication of the mention of the grant of a European patent or for 20 years from the date of filing if the application is refused or withdrawn or deemed to be withdrawn, the biological material deposited with the American Type Culture Collection under Accession No. see Attachment A

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

The indications listed below will be submitted to the International Bureau later *(specify the general nature of the indications e.g., "Accession Number of Deposit")*

For receiving Office use only	For International Bureau use only
☑ This sheet was received with the international application	☐ This sheet was received by the International Bureau on:
Authorized officer	Authorized officer

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM
(Additional Sheet)

C. ADDITIONAL INDICATIONS (Continued)

shall be made available as provided in ~~Rule 28(3) EPC only~~ by the issue of a sample to an expert nominated by the requester (Rule 28(4) EPC).

In respect of the designation of Australia in the subject PCT application, and in accordance with Regulation 3.25(3) of the Australian Patents Regulations, the Applicant hereby gives notice that the furnishing of a sample of the biological material deposited with the American Type Culture Collection under Accession No. See Attachment A shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention and who is nominated in a request for the furnishing of a sample.

In respect of the designation of Canada in the subject PCT application, the Applicant hereby informs the International Bureau that the Applicant wishes that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the biological material deposited with the American Type Culture Collection under Accession No. See Attachment A and referred to in the application to an independent expert nominated by the Commissioner.

Attachment A

Deposit of Clones

Clones AX65_22, BD335_14, BG241_1, BL187_4, BL249_18, BO71_1, BO365_2, BV51_1, BV140_3, BV141_2, CC194_4, and DA136_11 were deposited on October 3, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98196, from which each clone comprising a particular polynucleotide is obtainable.

Clones AR415_4, AS63_29, BG160_1, BO432_4, BO538_2, BR595_4, CI490_2, CI522_1, CN238_1, CO390_1, and AY304_1 (an additional isolate of clone AY304_14) were deposited on October 25, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98232, from which each clone comprising a particular polynucleotide is obtainable. Clone AY304_14 wasdeposited on October 23, 1997 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and was given the accession number 98561.

Clones AJ20_2, AR440_1, AS164_1, AX8_1, BD176_3, BD339_1, BD427_1, BL229_22, BV123_16, and CH377_1 were deposited on November 15, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98261, from which each clone comprising a particular polynucleotide is obtainable.

Clones BD441_1, BD441_2, BG102_3, BK158_1, BP163_1, BZ16_3, CC182_1, CG109_1 and CJ397_1 were deposited on November 20, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98264, from which each clone comprising a particular polynucleotide is obtainable.

Clones AM795_4, AT340_1, BG132_1, BG219_2, BG366_2, BV172_2, CC247_10, CI480_9, CO722_1, and CT748_2 were deposited on December 5, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98271, from which each clone comprising a particular polynucleotide is obtainable.

Clones AJ1_1, AQ73_3, BG142_1, BV66_1, BV291_3, CK201_1, CQ331_2, CT550_1, CT585_1 and CT797_3 were deposited on December 13, 1996 with the ATCC

Attachment A

(American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98278, from which each clone comprising a particular polynucleotide is obtainable.

Clones CB107_1, CG300_3, CJ145_1, CJ160_11, CO20_1, CO223_1, CO310_2, CP258_3, CW1155_3 and CZ247_2 were deposited on December 17, 1996 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98279, from which each clone comprising a particular polynucleotide is obtainable. Clone CO223_3 was deposited on January 9, 1997 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and was given the accession number 98291.

Clones AM666_1, BN387_3, BQ135_2, CR678_1, CW420_2, CW795_2, CW823_3, DF989_3, DL162_2, DL162_1, and EC172_1 were deposited on January 10, 1997 with the ATCC (American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number 98292, from which each clone comprising a particular polynucleotide is obtainable.

INTERNATIONAL SEARCH REPORT

International Application No
US 00/25135

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12N15/12 C07K14/47 C12N1/21 C12N5/10 C12Q1/68 A61K38/17

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, BIOSIS, STRAND

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X,L	WO 98 17687 A (GENETICS INST) 30 April 1998 (1998-04-30) the document throws doubt on the priority of the application abstract; claims 20-22 see SEQ ID NO: 8 and 9 (pp.73-77) page 18, line 30 -page 20, line 2 page 23, line 12 -page 24, line 14 page 31, line 12 -page 64, line 16 -----	1-11

☐ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

° Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
14 December 2000	30.01.01

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Oderwald, H

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-11

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-11

   An isolated polynucleotide comprising SEQ ID NO: 41 which encodes a protein of SEQ ID NO: 42 (BG160_1). A host cell, a process for producing said protein, a protein produced by said process, a composition comprising said protein.

2. Claims: 12, 13

   An isolated polynucleotide comprising SEQ ID NO: 129. A protein encoded by said polynucleotide having amico acid sequence SEQ ID NO: 130 (C0722_1).

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No
F US 00/25135

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9817687 A	30-04-1998	AU 5004097 A	15-05-1998
		EP 0960199 A	01-12-1999

each of such sequences may act as a transmembrane domain should that leader/signal sequence not be separated from the remainder of the AM795_4 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AM795_4 should be approximately 1900 bp.

The nucleotide sequence disclosed herein for AM795_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. AM795_4 demonstrated at least some similarity with sequences identified as AF002700 (Homo sapiens GDNF family receptor alpha 2 (GFRalpha2) mRNA, complete cds), H05619 (yl70a10.s1 Homo sapiens cDNA clone 43207 3'), U46493 (Cloning vector pFlp recombinase gene, complete cds), U59486 (Rattus norvegicus GDNF receptor alpha mRNA, complete cds), V00248 (Human Ret ligand retL2 cDNA), W73633 (zd55h01.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 344593 3', mRNA sequence), and W73681 (zd55h01.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 344593 5', mRNA sequence). The predicted amino acid sequence disclosed herein for AM795_4 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted AM795_4 protein demonstrated at least some similarity to sequences identified as AF002700 (GDNF family receptor alpha 2 (GFRalpha2) [Homo sapiens]), U59486 (GDNF receptor alpha [Rattus norvegicus]), and W37460 (Human Ret ligand retL2 cDNA). A receptor complex comprised of TrnR1 (GDNFR alpha) and Ret was found to be capable of mediating both GDNF and NTN signaling. The receptor called TrnR2, identified based on homology to TrnR1, is 48% identical to TrnR1 and is encoded by a gene located on the short arm of chromosome 8. TrnR2 is attached to the cell surface via a GPI-linkage, and can mediate both NTN and GDNF signaling through Ret *in vitro* (Baloh *et al.*, 1997, *Neuron* **18(5)**: 793-802, which is incorporated by reference herein). Based upon sequence similarity, AM795_4 proteins and each similar protein or peptide may share at least some activity.

AM795_4 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 76 kDa was detected in conditioned media fractions using SDS polyacrylamide gel electrophoresis.

Clone "AT340_1"

A polynucleotide of the present invention has been identified as clone "AT340_1". AT340_1 was isolated from a human adult blood (lymphocytes and dendritic cells treated with mixed lymphocyte reaction) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the

for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CJ397_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CJ397_1 protein").

The nucleotide sequence of the 5' portion of CJ397_1 as presently determined is reported in SEQ ID NO:107. An additional internal nucleotide sequence from CJ397_1 as presently determined is reported in SEQ ID NO:108. What applicants believe is the proper reading frame and the predicted amino acid sequence encoded by such internal sequence is reported in SEQ ID NO:109. Additional nucleotide sequence from the 3' portion of CJ397_1, including a poly(A) tail, is reported in SEQ ID NO:110.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CJ397_1 should be approximately 1900 bp.

The nucleotide sequence disclosed herein for CJ397_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CJ397_1 demonstrated at least some similarity with sequences identified as H18685 (yn52b08.s1 Homo sapiens cDNA clone 172023 3'), H46001 (yo13f06.s1 Homo sapiens cDNA clone 177827 3'), and T77612 (yc91f06.r1 Homo sapiens cDNA clone 23298 5'). Based upon sequence similarity, CJ397_1 proteins and each similar protein or peptide may share at least some activity.

Clone "AM795_4"

A polynucleotide of the present invention has been identified as clone "AM795_4". AM795_4 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. AM795_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AM795_4 protein").

The nucleotide sequence of AM795_4 as presently determined is reported in SEQ ID NO:111, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the AM795_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:112. Amino acids 9 to 21 of SEQ ID NO:112 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 22. Amino acids 138 to 150 of SEQ ID NO:112 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 151. Due to the hydrophobic nature of the predicted and the possible leader/signal sequences,

sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CC182_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CC182_1 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for CC182_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CC182_1 demonstrated at least some similarity with sequences identified as H61159 (yu37f08.s1 Homo sapiens cDNA clone 236007 3' similar to contains L1 repetitive element), L09709 (Human lysosomal-associated membrane glycoprotein-2 (LAMP2) gene, 5' end of CDS and flanking region), W44797 (zb98e10.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 320874 3' similar to contains Alu repetitive element), and X62167 (H.sapiens mRNA for P2 protein of peripheral myelin). Based upon sequence similarity, CC182_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of CC182_1 indicates that it may contain an L1 repetitive element and/or a MER42C repetitive element.

Clone "CG109_1"

A polynucleotide of the present invention has been identified as clone "CG109_1". CG109_1 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CG109_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CG109_1 protein").

The nucleotide sequence of CG109_1 as presently determined is reported in SEQ ID NO:105, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CG109_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:106.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CG109_1 should be approximately 600 bp.

The nucleotide sequence disclosed herein for CG109_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database.

Clone "CJ397_1"

A polynucleotide of the present invention has been identified as clone "CJ397_1". CJ397_1 was isolated from a human fetal brain cDNA library using methods which are selective

reported in SEQ ID NO:102. Additional nucleotide sequence from the 5' portion of BZ16_3 is reported in SEQ ID NO:100.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BZ16_3 should be approximately 2120 bp.

The nucleotide sequence disclosed herein for BZ16_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BZ16_3 demonstrated at least some similarity with sequences identified as F06886 (H. sapiens partial cDNA sequence; clone c-1nf02), F06870 (H. sapiens partial cDNA sequence; clone c-1ncl1), N53511 (yz26b08.s1 Homo sapiens cDNA clone 284151 3'), T65313 (yc79g12.s1 Homo sapiens cDNA clone 22132 3'), U00084 (Haemophilus influenzae), W44815 (zc21d01.s1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 322945 3'), and Z49128 (Caenorhabditis elegans cosmid M03C11). The predicted amino acid sequence disclosed herein for BZ16_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BZ16_3 protein demonstrated at least some similarity to sequences identified as D26185 (cell division protein [Bacillus subtilis]), L46096 (HEAHI1465_1 cell division protein [Haemophilus influenzae]), and Z49128 (CEM03C11_5 M03C11.5 [Caenorhabditis elegans]). The BZ16_3 protein demonstrated at least some similarity to ATP-dependent proteases such as ftsH. Based upon sequence similarity, BZ16_3 proteins and each similar protein or peptide may share at least some activity.

<u>Clone "CC182_1"</u>

A polynucleotide of the present invention has been identified as clone "CC182_1". CC182_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CC182_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CC182_1 protein").

The nucleotide sequence of CC182_1 as presently determined is reported in SEQ ID NO:103, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CC182_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:104. Amino acids 26 to 38 of SEQ ID NO:104 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 39. Due to the hydrophobic nature of the predicted leader/signal

of the encoded protein. BP163_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BP163_1 protein").

The nucleotide sequence of the 5' portion of BP163_1 as presently determined is reported in SEQ ID NO:97. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:98. The predicted amino acid sequence of the BP163_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:98. Additional nucleotide sequence from the 3' portion of BP163_1, including a poly(A) tail, is reported in SEQ ID NO:99.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BP163_1 should be approximately 1240 bp.

The nucleotide sequence disclosed herein for BP163_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BP163_1 demonstrated at least some similarity with sequences identified as AA187086 (zp58h06.r1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone 624443 5' similar to TR G285943 G285943 ORF, COMPLETE CDS), AA301506 (EST14475 Testis tumor Homo sapiens cDNA 5' end similar to hypothetical protein (GB D14659)), D14659 (Human mRNA for KIAA0103 gene, complete cds), and W57328 (ma26d10.r1 Life Tech mouse brain Mus musculus cDNA clone). The predicted amino acid sequence disclosed herein for BP163_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BP163_1 protein demonstrated at least some similarity to sequences identified as D14659 (KIAA0103 [Homo sapiens]). Based upon sequence similarity, BP163_1 proteins and each similar protein or peptide may share at least some activity.

Clone "BZ16_3"

A polynucleotide of the present invention has been identified as clone "BZ16_3". BZ16_3 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BZ16_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BZ16_3 protein").

The partial nucleotide sequence of BZ16_3, including its 3' end and a poly(A) tail, as presently determined is reported in SEQ ID NO:101. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:102. The predicted amino acid sequence of the BZ16_3 protein corresponding to the foregoing nucleotide sequence is

peptide may share at least some activity. The nucleotide sequence of BG102_3 indicates that it may contain an L1 repetitive element.

BG102_3 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 55 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

Clone "BK158_1"

A polynucleotide of the present invention has been identified as clone "BK158_1". BK158_1 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BK158_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BK158_1 protein").

The nucleotide sequence of BK158_1 as presently determined is reported in SEQ ID NO:95, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BK158_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:96.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BK158_1 should be approximately 1150 bp.

The nucleotide sequence disclosed herein for BK158_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BK158_1 demonstrated at least some similarity with sequences identified as N39195 (yv26e08.s1 Homo sapiens cDNA clone 243878 3') and N45263 (yv26e08.r1 Homo sapiens cDNA clone 243878 5'). Based upon sequence similarity, BK158_1 proteins and each similar protein or peptide may share at least some activity.

BK158_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 28 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "BP163_1"

A polynucleotide of the present invention has been identified as clone "BP163_1". BP163_1 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence

X61615 (leukemia inhibitory factor receptor [Homo sapiens]). Based upon sequence similarity, BD441_2 proteins and each similar protein or peptide may share at least some activity.

Clone "BG102_3"

A polynucleotide of the present invention has been identified as clone "BG102_3". BG102_3 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BG102_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BG102_3 protein").

The nucleotide sequence of BG102_3 as presently determined is reported in SEQ ID NO:93, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BG102_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:94. Amino acids 11 to 23 of SEQ ID NO:94 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 24. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the BG102_3 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BG102_3 should be approximately 1100 bp.

The nucleotide sequence disclosed herein for BG102_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BG102_3 demonstrated at least some similarity with sequences identified as AC002078 (Human BAC clone RG111H14 from 7q22, complete sequence), L11910 (Human retinoblastoma susceptibility gene exons 1-27, complete cds), U62317 (Chromosome 22q13 BAC Clone CIT987SK-384D8 complete sequence), Z54147 (Human DNA sequence from cosmid L129H7, Huntington's Disease Region, chromosome 4p16.3 contains CpG island), Z75747 (Human DNA sequence from cosmid U96H1, between markers DXS366 and DXS87 on chromosome X *), and Z80899 (Human DNA sequence from cosmid F1121 on chromosome 6). The predicted amino acid sequence disclosed herein for BG102_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BG102_3 protein demonstrated at least some similarity to sequences identified as M13100 (unknown protein [Rattus norvegicus]) and U15647 (reverse transcriptase [Mus musculus]). Based upon sequence similarity, BG102_3 proteins and each similar protein or

acid sequence of the encoded protein. BD441_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BD441_1 protein").

The nucleotide sequence of the 5' portion of BD441_1 as presently determined is reported in SEQ ID NO:86. An additional internal nucleotide sequence from BD441_1 as presently determined is reported in SEQ ID NO:87. What applicants believe is the proper reading frame and the predicted amino acid sequence encoded by such internal sequence is reported in SEQ ID NO:88. Additional nucleotide sequence from the 3' portion of BD441_1, including a poly(A) tail, is reported in SEQ ID NO:89.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BD441_1 should be approximately 2400 bp.

The predicted amino acid sequence disclosed herein for BD441_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BD441_1 protein demonstrated at least some similarity to sequences identified as X61615 (leukemia inhibitory factor receptor [Homo sapiens]). Based upon sequence similarity, BD441_1 proteins and each similar protein or peptide may share at least some activity.

Clone "BD441_2"

A polynucleotide of the present invention has been identified as clone "BD441_2". BD441_2 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BD441_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BD441_2 protein").

The nucleotide sequence of the 5' portion of BD441_2 as presently determined is reported in SEQ ID NO:90. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:91. The predicted amino acid sequence of the BD441_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:91. Additional nucleotide sequence from the 3' portion of BD441_2, including a poly(A) tail, is reported in SEQ ID NO:92.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BD441_2 should be approximately 1200 bp.

The predicted amino acid sequence disclosed herein for BD441_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BD441_2 protein demonstrated at least some similarity to sequences identified as

cDNA clone 198030 3'), U91321 (Human chromosome 16p13 BAC clone CIT987SK-363E6, complete sequence), and Z82200 (Human DNA sequence from clone J333E231). Based upon sequence similarity, BV123_16 proteins and each similar protein or peptide may share at least some activity.

Clone "CH377_1"

A polynucleotide of the present invention has been identified as clone "CH377_1". CH377_1 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CH377_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CH377_1 protein").

The nucleotide sequence of CH377_1 as presently determined is reported in SEQ ID NO:84, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CH377_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:85. Amino acids 5 to 17 of SEQ ID NO:85 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 18. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CH377_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CH377_1 should be approximately 570 bp.

The nucleotide sequence disclosed herein for CH377_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CH377_1 demonstrated at least some similarity with sequences identified as AA507382 (nh73b01.s1 NCI_CGAP_Br1.1 Homo sapiens cDNA clone IMAGE 964105) and N70479 (za74f12.s1 Homo sapiens cDNA clone 298319 3'). Based upon sequence similarity, CH377_1 proteins and each similar protein or peptide may share at least some activity.

Clone "BD441_1"

A polynucleotide of the present invention has been identified as clone "BD441_1". BD441_1 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino

acid sequence of the encoded protein. BL229_22 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BL229_22 protein").

The nucleotide sequence of the 5' portion of BL229_22 as presently determined is reported in SEQ ID NO:79. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:80. The predicted amino acid sequence of the BL229_22 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:80. Additional nucleotide sequence from the 3' portion of BL229_22, including a poly(A) tail, is reported in SEQ ID NO:81.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BL229_22 should be approximately 870 bp.

The nucleotide sequence disclosed herein for BL229_22 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database.

Clone "BV123_16"

A polynucleotide of the present invention has been identified as clone "BV123_16". BV123_16 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BV123_16 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BV123_16 protein").

The nucleotide sequence of BV123_16 as presently determined is reported in SEQ ID NO:82, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BV123_16 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:83.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BV123_16 should be approximately 1080 bp.

The nucleotide sequence disclosed herein for BV123_16 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BV123_16 demonstrated at least some similarity with sequences identified as H29610 (ym61e03.s1 Homo sapiens cDNA clone 52653 3'), H52374 (yq81b12.r1 Homo sapiens cDNA clone 202175 5'), H66213 (yu16h10.s1 Homo sapiens cDNA), L08092 (Homo sapiens dystrophin (DMD) gene, intron 7, transposon-like sequence), L35670 (Homo sapiens (subclone H8 10_g5 from P1 35 H5 C8) DNA sequence), M62716 (Human CSP-B gene flanking sequence), N46985 (yy83a05.s1 Homo sapiens cDNA clone 280112 3'), R94603 (yq38a04.s1 Homo sapiens

clone), U21730 Human 5'-nucleotidase (CD73)), W01979 (za30h09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 294113 5'), and W02015 (za32b11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 294237 5'). Based upon sequence similarity, BD339_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three potential transmembrane domains within the BD339_1 protein sequence, centered around amino acids 14, 46, and 76 of SEQ ID NO:76, respectively.

Clone "BD427_1"

A polynucleotide of the present invention has been identified as clone "BD427_1". BD427_1 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BD427_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BD427_1 protein").

The nucleotide sequence of BD427_1 as presently determined is reported in SEQ ID NO:77, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BD427_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:78.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BD427_1 should be approximately 1810 bp.

The nucleotide sequence disclosed herein for BD427_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BD427_1 demonstrated at least some similarity with sequences identified as BD427_1 demonstrated at least some similarity with sequences identified as AA027122 (zk04a03.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 469516 5'), N24735 (yx56b02.s1 Homo sapiens cDNA clone 265707 3'), and W84644 (zd91a06.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 356818 5'). Based upon sequence similarity, BD427_1 proteins and each similar protein or peptide may share at least some activity.

Clone "BL229_22"

A polynucleotide of the present invention has been identified as clone "BL229_22". BL229_22 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino

leader/signal sequence not be separated from the remainder of the BD176_3 protein. Additional nucleotide sequence from the 3' portion of BD176_3, including a poly(A) tail, is reported in SEQ ID NO:74.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BD176_3 should be approximately 1300 bp.

The nucleotide sequence disclosed herein for BD176_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BD176_3 demonstrated at least some similarity with sequences identified as AA029679 (ze94g10.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 366690 5'), D45913 (Mouse NLRR-1 mRNA for leucine-rich-repeat protein, complete cds), R55610 (yg88h08.r1 Homo sapiens cDNA clone 40606 5'), and T07640 (EST05530 Homo sapiens cDNA clone HFBEM16). The predicted amino acid sequence disclosed herein for BD176_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BD176_3 protein demonstrated at least some similarity to sequences identified as D45913 (leucine-rich-repeat protein [Mus musculus]) and M59472 (asparagine-rich antigen Pfa55-6 [Plasmodium falciparum]). Based upon sequence similarity, BD176_3 proteins and each similar protein or peptide may share at least some activity.

Clone "BD339_1"

A polynucleotide of the present invention has been identified as clone "BD339_1". BD339_1 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BD339_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BD339_1 protein").

The nucleotide sequence of BD339_1 as presently determined is reported in SEQ ID NO:75, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BD339_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:76.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BD339_1 should be approximately 650 bp.

The nucleotide sequence disclosed herein for BD339_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BD339_1 demonstrated at least some similarity with sequences identified as H82422 (yu80d08.s1 Homo sapiens cDNA clone 240111 3), N62058 (EST53c05 Homo sapiens cDNA

of the encoded protein. AX8_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AX8_1 protein").

The nucleotide sequence of AX8_1 as presently determined is reported in SEQ ID NO:70, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the AX8_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:71. Amino acids 106 to 118 of SEQ ID NO:71 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 119. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the AX8_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AX8_1 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for AX8_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database. The TopPredII computer program predicts three potential transmembrane domains within the AX8_1 protein sequence, centered around amino acids 111, 144, and 182 of SEQ ID NO:71, respectively.

AX8_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 35 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "BD176_3"

A polynucleotide of the present invention has been identified as clone "BD176_3". BD176_3 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BD176_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BD176_3 protein").

The nucleotide sequence of the 5' portion of BD176_3 as presently determined is reported in SEQ ID NO:72. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:73. The predicted amino acid sequence of the BD176_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:73. Amino acids 2 to 14 of SEQ ID NO:73 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 15. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted

A polynucleotide of the present invention has been identified as clone "AS164_1". AS164_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. AS164_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AS164_1 protein").

The nucleotide sequence of AS164_1 as presently determined is reported in SEQ ID NO:68, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the AS164_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:69.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AS164_1 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for AS164_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. AS164_1 demonstrated at least some similarity with sequences identified as H24668 (yl40h10.r1 Homo sapiens cDNA clone 160771 5'), N29757 (yw90h10.s1 Homo sapiens cDNA clone 259555 3'), T62184 (yb96d08.r1 Homo sapiens cDNA clone 79023 5'), Z69706 (Human DNA sequence from cosmid COS12 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs, Flanking sequences of 3' alpha globin H), and Z69890 (Human DNA sequence from cosmid RJ14 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs and CpG island). The predicted amino acid sequence disclosed herein for AS164_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted AS164_1 protein demonstrated at least some similarity to sequences identified as A20359_1 (ryanodine receptor gene product [Homo sapiens]) and U78866 (putative arginine-aspartate-rich RNA binding protein [Arabidopsis thaliana]). Based upon sequence similarity, AS164_1 proteins and each similar protein or peptide may share at least some activity. The predicted AS164_1 protein sequence also contains repeated Asp-Arg RNA-binding motifs.

Clone "AX8_1"

A polynucleotide of the present invention has been identified as clone "AX8_1". AX8_1 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence

region is indicated in SEQ ID NO:63. The predicted amino acid sequence of the AJ20_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:63. Amino acids 8 to 20 of SEQ ID NO:63 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 21. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the AJ20_2 protein. Additional nucleotide sequence from the 3' portion of AJ20_2, including a poly(A) tail, is reported in SEQ ID NO:64.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AJ20_2 should be approximately 850 bp.

The nucleotide sequence disclosed herein for AJ20_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database.

Clone "AR440_1"

A polynucleotide of the present invention has been identified as clone "AR440_1". AR440_1 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. AR440_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AR440_1 protein").

The partial nucleotide sequence of AR440_1, including its 3' end and a poly(A) tail, as presently determined is reported in SEQ ID NO:66. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:67. The predicted amino acid sequence of the AR440_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:67. Additional nucleotide sequence from the 5' portion of AR440_1 is reported in SEQ ID NO:65.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AR440_1 should be approximately 1400 bp.

The nucleotide sequence disclosed herein for AR440_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. No hits were found in the database. The nucleotide sequence of AR440_1 indicates that it may contain an Alu repetitive element.

Clone "AS164_1"

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CO390_1 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for CO390_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CO390_1 demonstrated at least some similarity with sequences identified as H84353 (yv85a11.r1 Homo sapiens cDNA clone 249500 5'), L35532 (Pan troglodytes Alu repeat region), N80616 (Genomic clone encoding SAP(Phe)), R53922 (yi03h10.s1 Homo sapiens cDNA clone 138211 3' similar to contains Alu repetitive element;contains TAR1 repetitive element), X75335 (H.sapiens Alu insertion in COL3A1 gene), X95882 (R.norvegicus mRNA for ATP ligand gated ion channel), and Y09561 (H.sapiens mRNA for P2X7 receptor). The predicted amino acid sequence disclosed herein for CO390_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CO390_1 protein demonstrated at least some sequence similarity with sequences identified as U45448 (P2x1 receptor [Homo sapiens]), W04216 (Rat superior cervical ganglion p2x receptor), X83688 (ATP receptor [Homo sapiens]), X95882 (P2X7 gene product [Rattus norvegicus]), and Y09561 (ATP receptor [Homo sapiens]). Based upon sequence similarity, CO390_1 proteins and each homologous protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the CO390_1 protein sequence, centered around amino acid 249 of SEQ ID NO:61. The nucleotide sequence of CO390_1 may contain an Alu repetitive element.

CO390_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 75 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

Clone "AJ20_2"

A polynucleotide of the present invention has been identified as clone "AJ20_2". AJ20_2 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. AJ20_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AJ20_2 protein").

The nucleotide sequence of the 5' portion of AJ20_2 as presently determined is reported in SEQ ID NO:62. What applicants presently believe is the proper reading frame for the coding

The nucleotide sequence of CN238_1 as presently determined is reported in SEQ ID NO:58, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CN238_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:59.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CN238_1 should be approximately 2190 bp.

The nucleotide sequence disclosed herein for CN238_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CN238_1 demonstrated at least some similarity with sequences identified as AA044097 (zk51b02.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 486315 5'), AA044287 (zk51b02.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 486315 3'), AA045440 (zk67c03.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 487876 3'), AA143007 (zl48f01.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 505177 5'), D51196 (Human fetal brain cDNA 3'-end GEN-016G05), D60310 (Human fetal brain cDNA 3'-end GEN-098A09), N69344 (yz43e04.s1 Homo sapiens cDNA clone 285822 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN)), W22250 (64B8 Human retina cDNA Tsp509I-cleaved sublibrary Homo), and X01703 (Human gene for alpha-tubulin (b alpha 1)). The predicted amino acid sequence disclosed herein for CN238_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CN238_1 protein demonstrated at least some sequence similarity with sequences identified as K00557 (alpha-tubulin [Homo sapiens]) and U51583 (zinc finger homeodomain enhancer-binding protein-1 [Rattus norvegicus]). Based upon sequence similarity, CN238_1 proteins and each homologous protein or peptide may share at least some activity.

Clone "CO390_1"

A polynucleotide of the present invention has been identified as clone "CO390_1". CO390_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CO390_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CO390_1 protein").

The nucleotide sequence of CO390_1 as presently determined is reported in SEQ ID NO:60, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CO390_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:61.

of the encoded protein. CI522_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CI522_1 protein").

The nucleotide sequence of the 5' portion of CI522_1 as presently determined is reported in SEQ ID NO:55. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:56. The predicted amino acid sequence of the CI522_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:56. Amino acids 7 to 19 of SEQ ID NO:56 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 20. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CI522_1 protein. Additional nucleotide sequence from the 3' portion of CI522_1, including a poly(A) tail, is reported in SEQ ID NO:57.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CI522_1 should be approximately 1400 bp.

The nucleotide sequence disclosed herein for CI522_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CI522_1 demonstrated at least some similarity with sequences identified as AA028557 (mi18g05.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone 463928 5'), H32238 (EST107136 Rattus sp. cDNA 5' end), T33525 (EST58140 Homo sapiens cDNA 5' end similar to None), U66468 (Human cell growth regulator CGR11 mRNA, complete cds), and X00525 (Mouse 28S ribosomal RNA). The predicted amino acid sequence disclosed herein for CI522_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CI522_1 protein demonstrated at least some sequence similarity with sequences identified as U66468 (cell growth regulator CGR11 [Homo sapiens]). Based upon sequence similarity, CI522_1 proteins and each homologous protein or peptide may share at least some activity.

Clone "CN238_1"

A polynucleotide of the present invention has been identified as clone "CN238_1". CN238_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CN238_1 includes at least a portion of the coding sequence of a secreted protein (also referred to herein as "CN238_1 protein").

foregoing nucleotide sequence is reported in SEQ ID NO:54. Amino acids 64 to 76 of SEQ ID NO:54 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 77. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CI490_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CI490_2 should be approximately 1200 bp.

The nucleotide sequence disclosed herein for CI490_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CI490_2 demonstrated at least some similarity with sequences identified as H30751 (yo79a04.r1 Homo sapiens cDNA clone 184110 5'), H49766 (yo24f01.r1 Homo sapiens cDNA clone 178873 5' similar to SP:S19586 N-METHYL-D-ASPARTATE RECEPTOR GLUTAMATE-BINDING CHAIN), H51158 (yo32d04.r1 Homo sapiens cDNA clone 179623 5'), R85211 (yo41d11.s1 Homo sapiens cDNA clone 180501 3' similar to SP S19586 N-METHYL-D-ASPARTATE RECEPTOR GLUTAMATE-BINDING CHAIN), S19586 (N-METHYL-D-ASPARTATE RECEPTOR GLUTAMATE-BINDING CHAIN), S61973 (NMDA receptor glutamate-binding subunit [rat, mRNA]), T01031 (Human leucine zipper protein-kinase cDNA sequence), and W56893 (zc01g05.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 321080 5' similar to PIR S19586 S19586 N-methyl-D-aspartate receptor glutamate-binding chain - rat). The predicted amino acid sequence disclosed herein for CI490_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CI490_2 protein demonstrated at least some sequence similarity with sequences identified as S61973 (NMDA receptor glutamate-binding subunit [Rattus sp.]) and U08020 (collagen pro-alpha-1 type I chain [Mus musculus]). Based upon sequence similarity, CI490_2 proteins and each homologous protein or peptide may share at least some activity. The TopPredII computer program predicts six potential transmembrane domains within the CI490_2 protein sequence, with the most amino-terminal transmembrane domain centered around amino acid 77 of SEQ ID NO:54.

Clone "CI522_1"

A polynucleotide of the present invention has been identified as clone "CI522_1". CI522_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence

Clone "BR595_4"

A polynucleotide of the present invention has been identified as clone "BR595_4". BR595_4 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BR595_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BR595_4 protein").

The nucleotide sequence of the 5' portion of BR595_4 as presently determined is reported in SEQ ID NO:50. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:51. The predicted amino acid sequence of the BR595_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:51. Additional nucleotide sequence from the 3' portion of BR595_4, including a poly(A) tail, is reported in SEQ ID NO:52.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BR595_4 should be approximately 3000 bp.

The nucleotide sequence disclosed herein for BR595_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BR595_4 demonstrated at least some similarity with sequences identified as AA443742 (zw95b02.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 784683 3'), AA600820 (np45b08.s1 NCI_CGAP_Br1.1 Homo sapiens cDNA clone IMAGE:1129239), T19410 (Human gene signature HUMGS00435), W87465 (zh67c04.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 417126 3'), and Z33587 (H. sapiens partial cDNA sequence; clone HEA89P; single read). Based upon sequence similarity, BR595_4 proteins and each homologous protein or peptide may share at least some activity.

Clone "CI490_2"

A polynucleotide of the present invention has been identified as clone "CI490_2". CI490_2 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. CI490_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CI490_2 protein").

The nucleotide sequence of CI490_2 as presently determined is reported in SEQ ID NO:53, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the CI490_2 protein corresponding to the

computer program predicts a potential transmembrane domain at the amino terminus of the BO432_4 protein sequence. The BO432_4 protein may also contain the bacterial lysR family signature, a motif found in bacterial transcriptional regulators and which is possibly indicative of a helix-turn-helix structure.

Clone "BO538_2"

A polynucleotide of the present invention has been identified as clone "BO538_2". BO538_2 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BO538_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BO538_2 protein").

The nucleotide sequence of the 5' portion of BO538_2 as presently determined is reported in SEQ ID NO:47. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:48. The predicted amino acid sequence of the BO538_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:48. Additional nucleotide sequence from the 3' portion of BO538_2, including a poly(A) tail, is reported in SEQ ID NO:49.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BO538_2 should be approximately 3000 bp.

The nucleotide sequence disclosed herein for BO538_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BO538_2 demonstrated at least some similarity with sequences identified as AA503100 (ne44h01.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone 900241), R44035 (yg21g09.s1 Homo sapiens cDNA clone 33167 3'), T21630 (Human gene signature HUMGS03066), and W64854 (me06d12.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 386711 5' similar to PIR S40989 S40989 hypothetical protein F55H2.6 - Caenorhabditis elegans). The predicted amino acid sequence disclosed herein for BO538_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BO538_2 protein demonstrated at least some sequence similarity with sequences identified as M60525 (nerve growth factor inducible protein [Rattus norvegicus]), R28916 (Type III procollagen), and Z27080 (F55H2.6 [Caenorhabditis elegans]). Based upon sequence similarity, BO538_2 proteins and each homologous protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the BO538_2 protein sequence.

program predicts three potential transmembrane domains within the BG160_1 protein sequence, centered around amino acids 84, 484, and 595 of SEQ ID NO:42, respectively.

BG160_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 110 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "BO432_4"

A polynucleotide of the present invention has been identified as clone "BO432_4". BO432_4 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BO432_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BO432_4 protein").

The nucleotide sequence of the 5' portion of BO432_4 as presently determined is reported in SEQ ID NO:43. An additional internal nucleotide sequence from BO432_4 as presently determined is reported in SEQ ID NO:44. What applicants believe is the proper reading frame and the predicted amino acid sequence encoded by such internal sequence is reported in SEQ ID NO:45. Additional nucleotide sequence from the 3' portion of BO432_4, including a poly(A) tail, is reported in SEQ ID NO:46.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BO432_4 should be approximately 1700 bp.

The nucleotide sequence disclosed herein for BO432_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BO432_4 demonstrated at least some similarity with sequences identified as AA283626 (zt15e09.s1 Soares NbHTGBC Homo sapiens cDNA clone 713224 3'), AA406486 (zv12g02.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 753458 5' similar to WP F35G2.2 CE05809 E.COLI YCAC LIKE), AA570446 (nk62c12.s1 NCI_CGAP_Sch1 Homo sapiens cDNA clone IMAGE:1018102), N55855 (J3389F Homo sapiens cDNA clone J3389 5'), Q10613 (Rianodin receptor gene), T62691 (yc70d10.r1 Homo sapiens cDNA clone 86035 5'), and W90766 (zh79h04.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 418327 3'). The predicted amino acid sequence disclosed herein for BO432_4 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BO432_4 protein demonstrated at least some sequence similarity with sequences identified as Z69637 (F35G2.2 [Caenorhabditis elegans]). Based upon sequence similarity, BO432_4 proteins and each homologous protein or peptide may share at least some activity. The TopPredII

A polynucleotide of the present invention has been identified as clone "BG160_1". BG160_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BG160_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BG160_1 protein").

The nucleotide sequence of BG160_1 as presently determined is reported in SEQ ID NO:41, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BG160_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:42. Amino acids 588 to 600 of SEQ ID NO:42 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 601. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the BG160_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BG160_1 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for BG160_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BG160_1 demonstrated at least some similarity with sequences identified as A60021 (tropomyosin-related protein, neuronal - rat ;contains element MER27 repetitive element), AA081525 (zn20e02.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone 547994 5'), AA092565 (115773.seq.F Fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'), D56138 (Human fetal brain cDNA 5'-end GEN-416H11), D61090 (Human fetal brain cDNA 5'-end GEN-155A07), D61184 (Human fetal brain cDNA 5'-end GEN-165A01), L10335 (Homo sapiens neuro-endocrine-specific protein C (NSP) mRNA, complete cds), N21304 (yx53f07.s1 Homo sapiens cDNA clone 265477 3' similar to SP:A60021 A60021 TROPOMYOSIN-RELATED PROTEIN, NEURONAL), and W95814 (ze07f11.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 358317 5' similar to PIR:A60021). The predicted amino acid sequence disclosed herein for BG160_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BG160_1 protein demonstrated at least some sequence similarity with sequences identified as L10334 (neuroendocrine-specific protein B [Homo sapiens]), L10335 (neuroendocrine-specific protein C [Homo sapiens]). Based upon sequence similarity, BG160_1 proteins and each homologous protein or peptide may share at least some activity. The TopPredII computer

A polynucleotide of the present invention has been identified as clone "AY304_14". AY304_14 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. AY304_14 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AY304_14 protein").

The nucleotide sequence of AY304_14 as presently determined is reported in SEQ ID NO:39, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the AY304_14 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:40.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AY304_14 should be approximately 2200 bp.

The nucleotide sequence disclosed herein for AY304_14 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. AY304_14 demonstrated at least some similarity with sequences identified as AA127688 (zk92f05.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490305 3'), AA179609 (zp49g11.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 612836 5'), AA276253 (vc40f05.r1 Barstead MPLRB1 Mus musculus cDNA clone 777057 5'), H15545 (ym27d04.s1 Homo sapiens cDNA clone 49495 3' similar to contains PTR5 repetitive element), L08441 (Human autonomously replicating sequence (ARS) mRNA), N34949 (yy49h09.s1 Homo sapiens cDNA clone 276929 3'), R48594 (yj65d07.s1 Homo sapiens cDNA clone 153613 3'), T21160 (Human gene signature HUMGS02466), U43284 (Cloning vector phGFP-S65T, complete sequence, green fluorescent protein (gfp) gene, complete cds), and Z45151 (H. sapiens partial cDNA sequence; clone c-2hh04). The predicted amino acid sequence disclosed herein for AY304_14 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted AY304_14 protein demonstrated at least some sequence similarity with sequences identified as D86984 (similar to yeast adenylate cyclase (S56776) [Homo sapiens]), J01415 (cytochrome oxidase subunit 3 [Homo sapiens]), V00662 (cytochrome oxidase III [Homo sapiens]), and X68948 (envelope glycoprotein [Spleen focus-forming virus]). Based upon sequence similarity, AY304_14 proteins and each homologous protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the AY304_14 protein sequence, one centered around amino acid 81 and another around amino acid 120 of SEQ ID NO:40.

Clone "BG160_1"

Clone "AS63_29"

A polynucleotide of the present invention has been identified as clone "AS63_29". AS63_29 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. AS63_29 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AS63_29 protein").

The nucleotide sequence of the 5' portion of AS63_29 as presently determined is reported in SEQ ID NO:36. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:37. The predicted amino acid sequence of the AS63_29 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:37. Amino acids 28 to 40 of SEQ ID NO:37 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 41. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the AS63_29 protein. Additional nucleotide sequence from the 3' portion of AS63_29, including a poly(A) tail, is reported in SEQ ID NO:38.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AS63_29 should be approximately 1700 bp.

The nucleotide sequence disclosed herein for AS63_29 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. AS63_29 demonstrated at least some similarity with sequences identified as L26877 (Mus musculus (B20c) heavy chain immunoglobulin variable region gene), T09146 (EST07039 Homo sapiens cDNA clone HIBBP68 5' end), T23466 (seq3050 Homo sapiens cDNA clone Hy18-Ch13-Charon40-cDNA-100 3'), and W55739 (ma35f05.r1 Life Tech mouse brain Mus musculus cDNA clone 312705 5'). The predicted amino acid sequence disclosed herein for AS63_29 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted AS63_29 protein demonstrated at least some sequence similarity with sequences identified as R04032 (Full length T4 encoded by plasmid pBG381). Based upon sequence similarity, AS63_29 proteins and each homologous protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the AS63_29 protein sequence, near the amino terminus.

Clone "AY304_14"

of the encoded protein. AR415_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AR415_4 protein").

The nucleotide sequence of AR415_4 as presently determined is reported in SEQ ID NO:34, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the AR415_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:35. Amino acids 14 to 26 of SEQ ID NO:35 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 27. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the AR415_4 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AR415_4 should be approximately 1500 bp.

The nucleotide sequence disclosed herein for AR415_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. AR415_4 demonstrated at least some similarity with sequences identified as AA100799 (zm26d01.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone 526753 3'), AA100852 (zm26d01.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone 526753 5' similar to SW CO02_HUMAN P19075 TUMOR-ASSOCIATED ANTIGEN CO-029), AA146605 (zo35c09.r1 Stratagene colon (#937204) Homo sapiens cDNA clone 588880 5' similar to SW:CO02_HUMAN P19075 TUMOR-ASSOCIATED ANTIGEN CO-029), AA224847 (nc33c12.s1 NCI CGAP Pr2 Homo sapiens cDNA clone 4079 similar to SW:CO02_HUMAN P19075 TUMOR-ASSOCIATED ANTIGEN CO-029), AA225191 (nc21h08.s1 NCI CGAP Pr1 Homo sapiens cDNA clone 2968), AA593864 (nn19f08.s1 NCI_CGAP_Co12 Homo sapiens cDNA clone IMAGE:1084359), D26483 (Mouse mRNA for PE31/TALLA), M33680 (Human 26-kDa cell surface protein TAPA-1 mRNA, complete cds), T14726 (Human CD53 antigen cDNA), and T23814 (Human gene signature HUMGS05723). The predicted amino acid sequence disclosed herein for AR415_4 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted AR415_4 protein demonstrated at least some sequence similarity with sequences identified as D29808 (TALLA-1 [Homo sapiens]), M35252 (tumor-associated antigen [Homo sapiens]), and R22360 (CO-029 tumour associated antigen protein). Based upon sequence similarity, AR415_4 proteins and each homologous protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the AR415_4 protein sequence centered around amino acid 100 of SEQ ID NO:35.

selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. DA136_11 includes at least a portion of the coding sequence of a secreted protein (also referred to herein as "DA136_11 protein").

The nucleotide sequence of DA136_11 as presently determined is reported in SEQ ID NO:32, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the DA136_11 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:33.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone DA136_11 should be approximately 3800 bp.

The nucleotide sequence disclosed herein for DA136_11 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. DA136_11 demonstrated at least some similarity with sequences identified as AA523414 (ng30a07.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone 936276), H89334 (yw25h09.r1 Homo sapiens cDNA clone 253313 5'), R59925 (yh11b12.s1 Homo sapiens cDNA clone 42891 3), T66165 (Human interleukin-12 receptor alpha chain NR4 DNA), Y09328 (H.sapiens mRNA for IL13 receptor alpha-1 chain), and Y10659 (H.sapiens IL-13Ra mRNA). The predicted amino acid sequence disclosed herein for DA136_11 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted DA136_11 protein demonstrated at least some similarity to sequences identified as L08960 (cell adhesion molecule [Gallus gallus]), M34083 (lactogen receptor precursor [Rattus norvegicus]), M59941 (GM-CSF receptor beta chain [Homo sapiens]), W09822 (Human interleukin-12 receptor alpha chain NR4), X61178 (interleukin-5 receptor type 3 [Homo sapiens]), and Y10659 (IL-13Ra [Homo sapiens]). Based upon sequence similarity, DA136_11 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the DA136_11 protein sequence, centered around amino acid 215 of SEQ ID NO:33.

<u>Clone "AR415_4"</u>

A polynucleotide of the present invention has been identified as clone "AR415_4". AR415_4 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence

of the encoded protein. CC194_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "CC194_4 protein").

The nucleotide sequence of the 5' portion of CC194_4 as presently determined is reported in SEQ ID NO:29. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:30. The predicted amino acid sequence of the CC194_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:30. Amino acids 88 to 100 of SEQ ID NO:30 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 101. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the CC194_4 protein. Additional nucleotide sequence from the 3' portion of CC194_4, including a poly(A) tail, is reported in SEQ ID NO:31.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone CC194_4 should be approximately 3300 bp.

The nucleotide sequence disclosed herein for CC194_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. CC194_4 demonstrated at least some similarity with sequences identified as AA722214 (zh20f10.s1 Soares pineal gland N3HPG Homo sapiens cDNA clone 412651 3', mRNA sequence), H11476 (ym10h08.s1 Homo sapiens cDNA clone 47781 3'), H11581 (ym10h08.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:47781 5' similar to SP:C36E8.3 CE00911; mRNA sequence), H23044 (ym51d07.r1 Homo sapiens cDNA clone 52058 5' similar to SP:C36E8.3 CE00911), N93789 (zb64g05.s1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 308408 3'), and W54544 (mc99a01.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus). The predicted amino acid sequence disclosed herein for CC194_4 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted CC194_4 protein demonstrated at least some similarity to sequences identified as M38561 (CAD [Homo sapiens]). Based upon sequence similarity, CC194_4 proteins and each similar protein or peptide may share at least some activity.

Clone "DA136_11"

A polynucleotide of the present invention has been identified as clone "DA136_11". DA136_11 was isolated from a human adult placenta cDNA library using methods which are

The nucleotide sequence disclosed herein for BV140_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BV140_3 demonstrated at least some similarity with sequences identified as H72799 (yu07d10.rl Homo sapiens cDNA clone 233107 5') and T94057 (ye33g08.rl Homo sapiens cDNA clone 119582 5'). Based upon sequence similarity, BV140_3 proteins and each similar protein or peptide may share at least some activity.

Clone "BV141_2"

A polynucleotide of the present invention has been identified as clone "BV141_2". BV141_2 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BV141_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BV141_2 protein").

The nucleotide sequence of BV141_2 as presently determined is reported in SEQ ID NO:27, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BV141_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:28.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BV141_2 should be approximately 1100 bp.

The nucleotide sequence disclosed herein for BV141_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BV141_2 demonstrated at least some similarity with sequences identified as L26860 (Mus musculus (C6e) heavy chain immunoglobulin variable region gene). Based upon sequence similarity, BV141_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the BV141_2 protein sequence, one centered around amino acid 34 and another around amino acid 65 of SEQ ID NO:28. The nucleotide sequence of BV141_2 indicates that it may contain one or more of the following repetitive element(s): L1 repeat.

Clone "CC194_4"

A polynucleotide of the present invention has been identified as clone "CC194_4". CC194_4 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence

The nucleotide sequence of the 5' portion of BV51_1 as presently determined is reported in SEQ ID NO:20. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:21. The predicted amino acid sequence of the BV51_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:21. Additional nucleotide sequence from the 3' portion of BV51_1, including a poly(A) tail, is reported in SEQ ID NO:22.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BV51_1 should be approximately 970 bp.

The nucleotide sequence disclosed herein for BV51_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BV51_1 demonstrated at least some similarity with sequences identified as AB012130 (Homo sapiens SBC2 mRNA for sodium bicarbonate cotransporter2, complete cds) and U46493 (Cloning vector pFlp recombinase gene, complete cds). The predicted amino acid sequence disclosed herein for BV51_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BV51_1 protein demonstrated at least some similarity to sequences identified as AB01213 (sodium bicarbonate cotransporter2 [Homo sapiens]). Based upon sequence similarity, BV51_1 proteins and each similar protein or peptide may share at least some activity.

Clone "BV140_3"

A polynucleotide of the present invention has been identified as clone "BV140_3". BV140_3 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BV140_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BV140_3 protein").

The nucleotide sequence of the 5' portion of BV140_3 as presently determined is reported in SEQ ID NO:23. An additional internal nucleotide sequence from BV140_3 as presently determined is reported in SEQ ID NO:24. What applicants believe is the proper reading frame and the predicted amino acid sequence encoded by such internal sequence is reported in SEQ ID NO:25. Additional nucleotide sequence from the 3' portion of BV140_3, including a poly(A) tail, is reported in SEQ ID NO:26.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BV140_3 should be approximately 3500 bp.

Clone "BO365_2"

A polynucleotide of the present invention has been identified as clone "BO365_2". BO365_2 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BO365_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BO365_2 protein").

The nucleotide sequence of BO365_2 as presently determined is reported in SEQ ID NO:18, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BO365_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:19.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BO365_2 should be approximately 2800 bp.

The nucleotide sequence disclosed herein for BO365_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BO365_2 demonstrated at least some similarity with sequences identified as D63876 (Human mRNA for KIAA0154 gene, partial cds) and Z83844 (Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 37E16; HTGS phase 1). The predicted amino acid sequence disclosed herein for BO365_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BO365_2 protein demonstrated at least some similarity to sequences identified as D10250 (alpha-fetoprotein enhancer binding protein [Homo sapiens]), D63876 (KIAA0154 gene product is related to mouse gamma adaptin [Homo sapiens]), and R23962 (AFP-1). Based upon sequence similarity, BO365_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three potential transmembrane domains within the BO365_2 protein sequence, centered around amino acids 70, 140, and 180 of SEQ ID NO:19, respectively.

Clone "BV51_1"

A polynucleotide of the present invention has been identified as clone "BV51_1". BV51_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BV51_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BV51_1 protein").

testis NHT Homo sapiens cDNA clone 726611 5'), R82633 (yj20a05.s1 Homo sapiens cDNA clone 149264 3'), and T22047 (Human gene signature HUMGS03590). The predicted amino acid sequence disclosed herein for BL249_18 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BL249_18 protein demonstrated at least some similarity to sequences identified as AC003673 (unknown protein (AAC09020.1) [Arabidopsis thaliana]) and Z98598 (hypothetical protein [Schizosaccharomyces pombe]). Based upon sequence similarity, BL249_18 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the BL249_18 protein sequence, one centered around amino acid 45 and another around amino acid 680 of SEQ ID NO:13.

Clone "BO71_1"

A polynucleotide of the present invention has been identified as clone "BO71_1". BO71_1 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BO71_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BO71_1 protein").

The nucleotide sequence of the 5' portion of BO71_1 as presently determined is reported in SEQ ID NO:14. An additional internal nucleotide sequence from BO71_1 as presently determined is reported in SEQ ID NO:15. What applicants believe is the proper reading frame and the predicted amino acid sequence encoded by such internal sequence is reported in SEQ ID NO:16. Additional nucleotide sequence from the 3' portion of BO71_1, including a poly(A) tail, is reported in SEQ ID NO:17.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BO71_1 should be approximately 2000 bp.

The nucleotide sequence disclosed herein for BO71_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BO71_1 demonstrated at least some similarity with sequences identified as X86809 (H.sapiens mRNA for major astrocytic phosphoprotein PEA-15). The predicted amino acid sequence disclosed herein for BO71_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted BO71_1 protein demonstrated at least some similarity to sequences identified as U06144 (cellular disintegrin-related protein [Mus musculus]). Based upon sequence similarity, BO71_1 proteins and each similar protein or peptide may share at least some activity.

sequence databases using the BLASTX search protocol. The predicted BL187_4 protein demonstrated at least some similarity to sequences identified as R95242 (HIC-1 polypeptide), Z19002 (kruppel-like zinc finger protein [Homo sapiens]), and a number of other zinc-finger proteins. Based upon sequence similarity, BL187_4 proteins and each similar protein or peptide may share at least some activity. Motifs analysis indicates the presence of two zinc-finger (C2H2 type) domains centered around amino acids 375 and 430 of SEQ ID NO:11, respectively. The TopPredII computer program predicts two potential transmembrane domains within the BL187_4 protein sequence, one centered around amino acid 30 and another around amino acid 260 of SEQ ID NO:11. BL187_4 protein appears to be a novel secreted or membrane-associated zinc-finger protein.

Clone "BL249_18"

A polynucleotide of the present invention has been identified as clone "BL249_18". BL249_18 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BL249_18 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BL249_18 protein").

The nucleotide sequence of BL249_18 as presently determined is reported in SEQ ID NO:12, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BL249_18 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:13. Amino acids 32 to 44 of SEQ ID NO:13 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 45. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the BL249_18 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BL249_18 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for BL249_18 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BL249_18 demonstrated at least some similarity with sequences identified as AA034864 (mi53f01.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 467257 5'), AA115100 (zl02h12.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 491207 3'), AA219365 (zr04c06.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 650506 5'), AA399095 (zt59b06.r1 Soares

least some similarity to sequences identified as Y12781 (transducin (beta) like 1 protein [Homo sapiens]) and other beta-transducin-like proteins (see GenBank accession numbers L28125 and T86738). Based upon sequence similarity, BG241_1 proteins and each similar protein or peptide may share at least some activity.

Clone "BL187_4"

A polynucleotide of the present invention has been identified as clone "BL187_4". BL187_4 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BL187_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BL187_4 protein").

The nucleotide sequence of BL187_4 as presently determined is reported in SEQ ID NO:10, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the BL187_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:11. Amino acids 17 to 29 of SEQ ID NO:11 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 30. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the BL187_4 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BL187_4 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for BL187_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BL187_4 demonstrated at least some similarity with sequences identified as AA476210 (zw35g01.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 771312 3', mRNA sequence), AA868505 (ak43b04.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE 1408687 3' similar to SW PLZF_HUMAN Q05516 ZINC FINGER PROTEIN PLZF; mRNA sequence), AA927876 (om18b09.s1 Soares NFL T GBC S1 Homo sapiens cDNA clone IMAGE:1541369 3', mRNA sequence), AD000671 (Homo sapiens DNA from chromosome 19-cosmid f24109 containing HRX2, genomic sequence), H48938 (EST0010 Homo sapiens cDNA clone HTN-6-15), and Z63958 (H.sapiens CpG DNA, clone 93d10, forward read cpg93d10.ft1a). The predicted amino acid sequence disclosed herein for BL187_4 was searched against the GenPept and GeneSeq amino acid

frame and the predicted amino acid sequence of the BD335_14 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:5.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BD335_14 should be approximately 3000 bp.

The nucleotide sequence disclosed herein for BD335_14 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. The predicted BD335_14 protein demonstrated at least some similarity with sequences identified as U83511 (APXL [Homo sapiens]). Based upon sequence similarity, BD335_14 proteins and each homologous protein or peptide may share at least some activity. The TopPredII computer program predicts three potential transmembrane domains within the BD335_14 protein sequence, one centered around amino acid 80, another around amino acid 320, and a third around amino acid 700 of SEQ ID NO:5.

Clone "BG241_1"

A polynucleotide of the present invention has been identified as clone "BG241_1". BG241_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BG241_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BG241_1 protein").

The nucleotide sequence of the 5' portion of BG241_1 as presently determined is reported in SEQ ID NO:6. An additional internal nucleotide sequence from BG241_1 as presently determined is reported in SEQ ID NO:7. What applicants believe is the proper reading frame and the predicted amino acid sequence encoded by such internal sequence is reported in SEQ ID NO:8. Additional nucleotide sequence from the 3' portion of BG241_1, including a poly(A) tail, is reported in SEQ ID NO:9.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone BG241_1 should be approximately 800 bp.

The nucleotide sequence disclosed herein for BG241_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. BG241_1 demonstrated at least some similarity with sequences identified as AI082187 (ox75f01.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE 1662169 3' similar to contains element MSR1 repetitive element; mRNA sequence), W38781 (zb27g08.r1 Soares parathyroid tumor NbHPA Homo sapiens), and Y12781 (Homo sapiens mRNA for transducin (beta) like 1 protein). The predicted BG241_1 protein demonstrated at

a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. AX65_22 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "AX65_22 protein").

The nucleotide sequence of the 5' portion of AX65_22 as presently determined is reported in SEQ ID NO:1. What applicants presently believe is the proper reading frame for the coding region is indicated in SEQ ID NO:2. The predicted amino acid sequence of the AX65_22 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:2. Amino acids 8 to 20 of SEQ ID NO:2 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 21. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the AX65_22 protein. Additional nucleotide sequence from the 3' portion of AX65_22, including a poly(A) tail, is reported in SEQ ID NO:3.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone AX65_22 should be approximately 3500 bp.

The nucleotide sequence disclosed herein for AX65_22 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. AX65_22 demonstrated at least some similarity with sequences identified as T08476 (Eukaryotic expression vector pAPEX-3p) and U46493 (Cloning vector pFlp recombinase gene, complete cds). The predicted AX65_22 protein demonstrated at least some homology with sequences identified as J01969 (DNA polymerase [Human adenovirus type 5]), R07640 (Deduced protein sequence of p170-2

comprising T4), and X57205 (fibroblast growth factor receptor [Homo sapiens]). Based upon sequence similarity, AX65_22 proteins and each similar protein or peptide may share at least some activity.

Clone "BD335_14"

A polynucleotide of the present invention has been identified as clone "BD335_14". BD335_14 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. BD335_14 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "BD335_14 protein").

The nucleotide sequence of BD335_14 as presently determined is reported in SEQ ID NO:4, and includes a poly(A) tail. What applicants presently believe to be the proper reading

The protein produced according to such methods is also provided by the present invention.

Protein compositions of the present invention may further comprise a pharmaceutically acceptable carrier. Compositions comprising an antibody which specifically reacts with such protein are also provided by the present invention.

Methods are also provided for preventing, treating or ameliorating a medical condition which comprises administering to a mammalian subject a therapeutically effective amount of a composition comprising a protein of the present invention and a pharmaceutically acceptable carrier.

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A and 1B are schematic representations of the pED6 and pNOTs vectors, respectively, used for deposit of clones disclosed herein.

DETAILED DESCRIPTION

ISOLATED PROTEINS AND POLYNUCLEOTIDES

Nucleotide and amino acid sequences, as presently determined, are reported below for each clone and protein disclosed in the present application. The nucleotide sequence of each clone can readily be determined by sequencing of the deposited clone in accordance with known methods. The predicted amino acid sequence (both full-length and mature forms) can then be determined from such nucleotide sequence. The amino acid sequence of the protein encoded by a particular clone can also be determined by expression of the clone in a suitable host cell, collecting the protein and determining its sequence. For each disclosed protein applicants have identified what they have determined to be the reading frame best identifiable with sequence information available at the time of filing.

As used herein a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g. , receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplasmic reticulum.

Clone "AX65_22"

A polynucleotide of the present invention has been identified as clone "AX65_22". AX65_22 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding

nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:198 from nucleotide 2130 to nucleotide 2600, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:198 from nucleotide 2130 to nucleotide 2600. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:198 from nucleotide 1 to nucleotide 506, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:198 from nucleotide 1 to nucleotide 506, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:198 from nucleotide 1 to nucleotide 506.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:199;

(b) the amino acid sequence of SEQ ID NO:199 from amino acid 1 to amino acid 130;

(c) a fragment of the amino acid sequence of SEQ ID NO:199, the fragment comprising eight contiguous amino acids of SEQ ID NO:199; and

(d) the amino acid sequence encoded by the cDNA insert of clone EC172_1 deposited with the ATCC under accession number 98292;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:199 or the amino acid sequence of SEQ ID NO:199 from amino acid 1 to amino acid 130. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:199 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:199, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:199 having biological activity, the fragment comprising the amino acid sequence from amino acid 409 to amino acid 418 of SEQ ID NO:199.

In certain preferred embodiments, the polynucleotide is operably linked to an expression control sequence. The invention also provides a host cell, including bacterial, yeast, insect and mammalian cells, transformed with such polynucleotide compositions. Also provided by the present invention are organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein.

Processes are also provided for producing a protein, which comprise:

(a) growing a culture of the host cell transformed with such polynucleotide compositions in a suitable culture medium; and

(b) purifying the protein from the culture.

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:198, but excluding the poly(A) tail at the 3' end of SEQ ID NO:198; and

(ab) the nucleotide sequence of the cDNA insert of clone EC172_1 deposited with the ATCC under accession number 98292;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:198, but excluding the poly(A) tail at the 3' end of SEQ ID NO:198; and

(bb) the nucleotide sequence of the cDNA insert of clone EC172_1 deposited with the ATCC under accession number 98292;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:198, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:198 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:198 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:198. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:198 from nucleotide 117 to nucleotide 2600, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:198 from nucleotide 117 to nucleotide 2600, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:198 from nucleotide 117 to nucleotide 2600. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:198 from nucleotide 2130 to nucleotide 2600, and extending contiguously from a

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:199 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:199;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:198.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:198 from nucleotide 117 to nucleotide 2600; the nucleotide sequence of SEQ ID NO:198 from nucleotide 2130 to nucleotide 2600; the nucleotide sequence of SEQ ID NO:198 from nucleotide 1 to nucleotide 506; the nucleotide sequence of the full-length protein coding sequence of clone EC172_1 deposited with the ATCC under accession number 98292; or the nucleotide sequence of a mature protein coding sequence of clone EC172_1 deposited with the ATCC under accession number 98292. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone EC172_1 deposited with the ATCC under accession number 98292. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:199 from amino acid 1 to amino acid 130. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:199 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:199, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:199 having biological activity, the fragment comprising the amino acid sequence from amino acid 409 to amino acid 418 of SEQ ID NO:199.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:198.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(c) a fragment of the amino acid sequence of SEQ ID NO:197, the fragment comprising eight contiguous amino acids of SEQ ID NO:197; and

(d) the amino acid sequence encoded by the cDNA insert of clone DL162_2 deposited with the ATCC under accession number 98292;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:197 or the amino acid sequence of SEQ ID NO:197 from amino acid 860 to amino acid 1066. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:197 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:197, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:197 having biological activity, the fragment comprising the amino acid sequence from amino acid 532 to amino acid 541 of SEQ ID NO:197.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:198;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:198 from nucleotide 117 to nucleotide 2600;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:198 from nucleotide 2130 to nucleotide 2600;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:198 from nucleotide 1 to nucleotide 506;

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone EC172_1 deposited with the ATCC under accession number 98292;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone EC172_1 deposited with the ATCC under accession number 98292;

(g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone EC172_1 deposited with the ATCC under accession number 98292;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone EC172_1 deposited with the ATCC under accession number 98292;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:199;

(ba) SEQ ID NO:196, but excluding the poly(A) tail at the 3' end of SEQ ID NO:196; and

(bb) the nucleotide sequence of the cDNA insert of clone DL162_2 deposited with the ATCC under accession number 98292;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:196, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:196 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:196 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:196. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:196 from nucleotide 121 to nucleotide 3345, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:196 from nucleotide 121 to nucleotide 3345, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:196 from nucleotide 121 to nucleotide 3345. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:196 from nucleotide 160 to nucleotide 3345, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:196 from nucleotide 160 to nucleotide 3345, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:196 from nucleotide 160 to nucleotide 3345. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:196 from nucleotide 2592 to nucleotide 3318, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:196 from nucleotide 2592 to nucleotide 3318, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:196 from nucleotide 2592 to nucleotide 3318.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:197;

(b) the amino acid sequence of SEQ ID NO:197 from amino acid 860 to amino acid 1066;

nucleotide 160 to nucleotide 3345; the nucleotide sequence of SEQ ID NO:196 from nucleotide 2592 to nucleotide 3318; the nucleotide sequence of the full-length protein coding sequence of clone DL162_2 deposited with the ATCC under accession number 98292; or the nucleotide sequence of a mature protein coding sequence of clone DL162_2 deposited with the ATCC under accession number 98292. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone DL162_2 deposited with the ATCC under accession number 98292. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:197 from amino acid 860 to amino acid 1066. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:197 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:197, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:197 having biological activity, the fragment comprising the amino acid sequence from amino acid 532 to amino acid 541 of SEQ ID NO:197.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:196.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:196, but excluding the poly(A) tail at the 3' end of SEQ ID NO:196; and

(ab) the nucleotide sequence of the cDNA insert of clone DL162_2 deposited with the ATCC under accession number 98292;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:196;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:196 from nucleotide 121 to nucleotide 3345;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:196 from nucleotide 160 to nucleotide 3345;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:196 from nucleotide 2592 to nucleotide 3318;

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone DL162_2 deposited with the ATCC under accession number 98292;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone DL162_2 deposited with the ATCC under accession number 98292;

(g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone DL162_2 deposited with the ATCC under accession number 98292;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone DL162_2 deposited with the ATCC under accession number 98292;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:197;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:197 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:197;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:196.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:196 from nucleotide 121 to nucleotide 3345; the nucleotide sequence of SEQ ID NO:196 from

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:194, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:194 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:194 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:194. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:194 from nucleotide 251 to nucleotide 787, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:194 from nucleotide 251 to nucleotide 787, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:194 from nucleotide 251 to nucleotide 787. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:194 from nucleotide 371 to nucleotide 787, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:194 from nucleotide 371 to nucleotide 787, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:194 from nucleotide 371 to nucleotide 787.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:195;

(b) the amino acid sequence of SEQ ID NO:195 from amino acid 38 to amino acid 170;

(c) a fragment of the amino acid sequence of SEQ ID NO:195, the fragment comprising eight contiguous amino acids of SEQ ID NO:195; and

(d) the amino acid sequence encoded by the cDNA insert of clone DL162_1 deposited with the ATCC under accession number 98292;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:195 or the amino acid sequence of SEQ ID NO:195 from amino acid 38 to amino acid 170. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:195 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:195, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:195 having biological activity, the fragment comprising the amino acid sequence from amino acid 84 to amino acid 93 of SEQ ID NO:195.

deposited with the ATCC under accession number 98292. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:195 from amino acid 38 to amino acid 170. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:195 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:195, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:195 having biological activity, the fragment comprising the amino acid sequence from amino acid 84 to amino acid 93 of SEQ ID NO:195.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:194.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:194, but excluding the poly(A) tail at the 3' end of SEQ ID NO:194; and

(ab) the nucleotide sequence of the cDNA insert of clone DL162_1 deposited with the ATCC under accession number 98292;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:194, but excluding the poly(A) tail at the 3' end of SEQ ID NO:194; and

(bb) the nucleotide sequence of the cDNA insert of clone DL162_1 deposited with the ATCC under accession number 98292;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:194 from nucleotide 251 to nucleotide 787;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:194 from nucleotide 371 to nucleotide 787;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone DL162_1 deposited with the ATCC under accession number 98292;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone DL162_1 deposited with the ATCC under accession number 98292;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone DL162_1 deposited with the ATCC under accession number 98292;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone DL162_1 deposited with the ATCC under accession number 98292;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:195;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:195 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:195;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:194.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:194 from nucleotide 251 to nucleotide 787; the nucleotide sequence of SEQ ID NO:194 from nucleotide 371 to nucleotide 787; the nucleotide sequence of the full-length protein coding sequence of clone DL162_1 deposited with the ATCC under accession number 98292; or the nucleotide sequence of a mature protein coding sequence of clone DL162_1 deposited with the ATCC under accession number 98292. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone DL162_1

according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:191, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:191 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:191. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:191 from nucleotide 548 to nucleotide 868, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:191 from nucleotide 548 to nucleotide 868, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:191 from nucleotide 548 to nucleotide 868. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:191 from nucleotide 590 to nucleotide 868, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:191 from nucleotide 590 to nucleotide 868, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:191 from nucleotide 590 to nucleotide 868.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:192;

(b) the amino acid sequence of SEQ ID NO:192 from amino acid 75 to amino acid 107;

(c) a fragment of the amino acid sequence of SEQ ID NO:192, the fragment comprising eight contiguous amino acids of SEQ ID NO:192; and

(d) the amino acid sequence encoded by the cDNA insert of clone DF989_3 deposited with the ATCC under accession number 98292;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:192 or the amino acid sequence of SEQ ID NO:192 from amino acid 75 to amino acid 107. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:192 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:192, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:192 having biological activity, the fragment comprising the amino acid sequence from amino acid 48 to amino acid 57 of SEQ ID NO:192.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:194;

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:191 and SEQ ID NO:193.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:191;

(ab) SEQ ID NO:193, but excluding the poly(A) tail at the 3' end of SEQ ID NO:193; and

(ac) the nucleotide sequence of the cDNA insert of clone DF989_3 deposited with the ATCC under accession number 98292;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:191;

(bb) SEQ ID NO:193, but excluding the poly(A) tail at the 3' end of SEQ ID NO:193; and

(bc) the nucleotide sequence of the cDNA insert of clone DF989_3 deposited with the ATCC under accession number 98292;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:191 and SEQ ID NO:193, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:191 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:193, but excluding the poly(A) tail at the 3' end of SEQ ID NO:193. Also preferably the polynucleotide isolated

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone DF989_3 deposited with the ATCC under accession number 98292;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone DF989_3 deposited with the ATCC under accession number 98292;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:192;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:192 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:192;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:191.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:191 from nucleotide 548 to nucleotide 868; the nucleotide sequence of SEQ ID NO:191 from nucleotide 590 to nucleotide 868; the nucleotide sequence of the full-length protein coding sequence of clone DF989_3 deposited with the ATCC under accession number 98292; or the nucleotide sequence of a mature protein coding sequence of clone DF989_3 deposited with the ATCC under accession number 98292. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone DF989_3 deposited with the ATCC under accession number 98292. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:192 from amino acid 75 to amino acid 107. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:192 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:192, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:192 having biological activity, the fragment comprising the amino acid sequence from amino acid 48 to amino acid 57 of SEQ ID NO:192.

from nucleotide 401 to nucleotide 589. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:189 from nucleotide 258 to nucleotide 627, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:189 from nucleotide 258 to nucleotide 627, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:189 from nucleotide 258 to nucleotide 627.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:190;

(b) a fragment of the amino acid sequence of SEQ ID NO:190, the fragment comprising eight contiguous amino acids of SEQ ID NO:190; and

(c) the amino acid sequence encoded by the cDNA insert of clone CW823_3 deposited with the ATCC under accession number 98292;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:190. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:190 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:190, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:190 having biological activity, the fragment comprising the amino acid sequence from amino acid 26 to amino acid 35 of SEQ ID NO:190.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:191;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:191 from nucleotide 548 to nucleotide 868;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:191 from nucleotide 590 to nucleotide 868;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone DF989_3 deposited with the ATCC under accession number 98292;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone DF989_3 deposited with the ATCC under accession number 98292;

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:189, but excluding the poly(A) tail at the 3' end of SEQ ID NO:189; and

(ab) the nucleotide sequence of the cDNA insert of clone CW823_3 deposited with the ATCC under accession number 98292;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:189, but excluding the poly(A) tail at the 3' end of SEQ ID NO:189; and

(bb) the nucleotide sequence of the cDNA insert of clone CW823_3 deposited with the ATCC under accession number 98292;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:189, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:189 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:189 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:189. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:189 from nucleotide 401 to nucleotide 589, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:189 from nucleotide 401 to nucleotide 589, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:189

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CW823_3 deposited with the ATCC under accession number 98292;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CW823_3 deposited with the ATCC under accession number 98292;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:190;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:190 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:190;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:189.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:189 from nucleotide 401 to nucleotide 589; the nucleotide sequence of SEQ ID NO:189 from nucleotide 258 to nucleotide 627; the nucleotide sequence of the full-length protein coding sequence of clone CW823_3 deposited with the ATCC under accession number 98292; or the nucleotide sequence of a mature protein coding sequence of clone CW823_3 deposited with the ATCC under accession number 98292. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CW823_3 deposited with the ATCC under accession number 98292. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:190 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:190, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:190 having biological activity, the fragment comprising the amino acid sequence from amino acid 26 to amino acid 35 of SEQ ID NO:190.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:189.

nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:187 from nucleotide 1 to nucleotide 529, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:187 from nucleotide 1 to nucleotide 529.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:188;

(b) the amino acid sequence of SEQ ID NO:188 from amino acid 1 to amino acid 137;

(c) a fragment of the amino acid sequence of SEQ ID NO:188, the fragment comprising eight contiguous amino acids of SEQ ID NO:188; and

(d) the amino acid sequence encoded by the cDNA insert of clone CW795_2 deposited with the ATCC under accession number 98292;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:188 or the amino acid sequence of SEQ ID NO:188 from amino acid 1 to amino acid 137. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:188 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:188, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:188 having biological activity, the fragment comprising the amino acid sequence from amino acid 338 to amino acid 347 of SEQ ID NO:188.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:189;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:189 from nucleotide 401 to nucleotide 589;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:189 from nucleotide 258 to nucleotide 627;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CW823_3 deposited with the ATCC under accession number 98292;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CW823_3 deposited with the ATCC under accession number 98292;

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:187, but excluding the poly(A) tail at the 3' end of SEQ ID NO:187; and

(ab) the nucleotide sequence of the cDNA insert of clone CW795_2 deposited with the ATCC under accession number 98292;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:187, but excluding the poly(A) tail at the 3' end of SEQ ID NO:187; and

(bb) the nucleotide sequence of the cDNA insert of clone CW795_2 deposited with the ATCC under accession number 98292;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:187, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:187 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:187 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:187. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:187 from nucleotide 119 to nucleotide 2176, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:187 from nucleotide 119 to nucleotide 2176, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:187 from nucleotide 119 to nucleotide 2176. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:187 from nucleotide 1 to nucleotide 529, and extending contiguously from a

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:188 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:188;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:187.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:187 from nucleotide 119 to nucleotide 2176; the nucleotide sequence of SEQ ID NO:187 from nucleotide 1 to nucleotide 529; the nucleotide sequence of the full-length protein coding sequence of clone CW795_2 deposited with the ATCC under accession number 98292; or the nucleotide sequence of a mature protein coding sequence of clone CW795_2 deposited with the ATCC under accession number 98292. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CW795_2 deposited with the ATCC under accession number 98292. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:188 from amino acid 1 to amino acid 137. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:188 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:188, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:188 having biological activity, the fragment comprising the amino acid sequence from amino acid 338 to amino acid 347 of SEQ ID NO:188.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:187.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(a) the amino acid sequence of SEQ ID NO:186;

(b) the amino acid sequence of SEQ ID NO:186 from amino acid 370 to amino acid 532;

(c) a fragment of the amino acid sequence of SEQ ID NO:186, the fragment comprising eight contiguous amino acids of SEQ ID NO:186; and

(d) the amino acid sequence encoded by the cDNA insert of clone CW420_2 deposited with the ATCC under accession number 98292;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:186 or the amino acid sequence of SEQ ID NO:186 from amino acid 370 to amino acid 532. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:186 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:186, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:186 having biological activity, the fragment comprising the amino acid sequence from amino acid 725 to amino acid 734 of SEQ ID NO:186.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:187;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:187 from nucleotide 119 to nucleotide 2176;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:187 from nucleotide 1 to nucleotide 529;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CW795_2 deposited with the ATCC under accession number 98292;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CW795_2 deposited with the ATCC under accession number 98292;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CW795_2 deposited with the ATCC under accession number 98292;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CW795_2 deposited with the ATCC under accession number 98292;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:188;

(ab) the nucleotide sequence of the cDNA insert of clone CW420_2 deposited with the ATCC under accession number 98292;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:185, but excluding the poly(A) tail at the 3' end of SEQ ID NO:185; and

(bb) the nucleotide sequence of the cDNA insert of clone CW420_2 deposited with the ATCC under accession number 98292;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:185, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:185 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:185 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:185. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:185 from nucleotide 116 to nucleotide 4498, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:185 from nucleotide 116 to nucleotide 4498, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:185 from nucleotide 116 to nucleotide 4498. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:185 from nucleotide 1221 to nucleotide 1711, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:185 from nucleotide 1221 to nucleotide 1711, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:185 from nucleotide 1221 to nucleotide 1711.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:185.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:185 from nucleotide 116 to nucleotide 4498; the nucleotide sequence of SEQ ID NO:185 from nucleotide 1221 to nucleotide 1711; the nucleotide sequence of the full-length protein coding sequence of clone CW420_2 deposited with the ATCC under accession number 98292; or the nucleotide sequence of a mature protein coding sequence of clone CW420_2 deposited with the ATCC under accession number 98292. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CW420_2 deposited with the ATCC under accession number 98292. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:186 from amino acid 370 to amino acid 532. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:186 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:186, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:186 having biological activity, the fragment comprising the amino acid sequence from amino acid 725 to amino acid 734 of SEQ ID NO:186.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:185.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:185, but excluding the poly(A) tail at the 3' end of SEQ ID NO:185; and

(c) a fragment of the amino acid sequence of SEQ ID NO:184, the fragment comprising eight contiguous amino acids of SEQ ID NO:184; and

(d) the amino acid sequence encoded by the cDNA insert of clone CR678_1 deposited with the ATCC under accession number 98292;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:184 or the amino acid sequence of SEQ ID NO:184 from amino acid 1 to amino acid 106. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:184 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:184, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:184 having biological activity, the fragment comprising the amino acid sequence from amino acid 78 to amino acid 87 of SEQ ID NO:184.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:185;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:185 from nucleotide 116 to nucleotide 4498;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:185 from nucleotide 1221 to nucleotide 1711;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CW420_2 deposited with the ATCC under accession number 98292;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CW420_2 deposited with the ATCC under accession number 98292;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CW420_2 deposited with the ATCC under accession number 98292;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CW420_2 deposited with the ATCC under accession number 98292;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:186;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:186 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:186;

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:183, but excluding the poly(A) tail at the 3' end of SEQ ID NO:183; and

(bb) the nucleotide sequence of the cDNA insert of clone CR678_1 deposited with the ATCC under accession number 98292;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:183, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:183 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:183 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:183. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:183 from nucleotide 214 to nucleotide 714, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:183 from nucleotide 214 to nucleotide 714, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:183 from nucleotide 214 to nucleotide 714. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:183 from nucleotide 151 to nucleotide 531, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:183 from nucleotide 151 to nucleotide 531, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:183 from nucleotide 151 to nucleotide 531.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:184;

(b) the amino acid sequence of SEQ ID NO:184 from amino acid 1 to amino acid 106;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:183.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:183 from nucleotide 214 to nucleotide 714; the nucleotide sequence of SEQ ID NO:183 from nucleotide 151 to nucleotide 531; the nucleotide sequence of the full-length protein coding sequence of clone CR678_1 deposited with the ATCC under accession number 98292; or the nucleotide sequence of a mature protein coding sequence of clone CR678_1 deposited with the ATCC under accession number 98292. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CR678_1 deposited with the ATCC under accession number 98292. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:184 from amino acid 1 to amino acid 106. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:184 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:184, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:184 having biological activity, the fragment comprising the amino acid sequence from amino acid 78 to amino acid 87 of SEQ ID NO:184.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:183.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:183, but excluding the poly(A) tail at the 3' end of SEQ ID NO:183; and

(ab) the nucleotide sequence of the cDNA insert of clone CR678_1 deposited with the ATCC under accession number 98292;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:182 or the amino acid sequence of SEQ ID NO:182 from amino acid 1 to amino acid 93. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:182 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:182, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:182 having biological activity, the fragment comprising the amino acid sequence from amino acid 99 to amino acid 108 of SEQ ID NO:182.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:183;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:183 from nucleotide 214 to nucleotide 714;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:183 from nucleotide 151 to nucleotide 531;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CR678_1 deposited with the ATCC under accession number 98292;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CR678_1 deposited with the ATCC under accession number 98292;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CR678_1 deposited with the ATCC under accession number 98292;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CR678_1 deposited with the ATCC under accession number 98292;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:184;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:184 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:184;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:181, but excluding the poly(A) tail at the 3' end of SEQ ID NO:181; and

(bb) the nucleotide sequence of the cDNA insert of clone BQ135_2 deposited with the ATCC under accession number 98292;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:181, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:181 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:181 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:181. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:181 from nucleotide 139 to nucleotide 765, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:181 from nucleotide 139 to nucleotide 765, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:181 from nucleotide 139 to nucleotide 765. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:181 from nucleotide 1 to nucleotide 416, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:181 from nucleotide 1 to nucleotide 416, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:181 from nucleotide 1 to nucleotide 416.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:182;

(b) the amino acid sequence of SEQ ID NO:182 from amino acid 1 to amino acid 93;

(c) a fragment of the amino acid sequence of SEQ ID NO:182, the fragment comprising eight contiguous amino acids of SEQ ID NO:182; and

(d) the amino acid sequence encoded by the cDNA insert of clone BQ135_2 deposited with the ATCC under accession number 98292;

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:181 from nucleotide 139 to nucleotide 765; the nucleotide sequence of SEQ ID NO:181 from nucleotide 1 to nucleotide 416; the nucleotide sequence of the full-length protein coding sequence of clone BQ135_2 deposited with the ATCC under accession number 98292; or the nucleotide sequence of a mature protein coding sequence of clone BQ135_2 deposited with the ATCC under accession number 98292. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BQ135_2 deposited with the ATCC under accession number 98292. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:182 from amino acid 1 to amino acid 93. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:182 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:182, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:182 having biological activity, the fragment comprising the amino acid sequence from amino acid 99 to amino acid 108 of SEQ ID NO:182.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:181.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:181, but excluding the poly(A) tail at the 3' end of SEQ ID NO:181; and

(ab) the nucleotide sequence of the cDNA insert of clone BQ135_2 deposited with the ATCC under accession number 98292;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

comprising a fragment of the amino acid sequence of SEQ ID NO:180 having biological activity, the fragment comprising the amino acid sequence from amino acid 21 to amino acid 30 of SEQ ID NO:180.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:181;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:181 from nucleotide 139 to nucleotide 765;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:181 from nucleotide 1 to nucleotide 416;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BQ135_2 deposited with the ATCC under accession number 98292;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BQ135_2 deposited with the ATCC under accession number 98292;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BQ135_2 deposited with the ATCC under accession number 98292;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BQ135_2 deposited with the ATCC under accession number 98292;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:182;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:182 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:182;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:181.

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:179, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:179 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:179 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:179. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:179 from nucleotide 751 to nucleotide 906, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:179 from nucleotide 751 to nucleotide 906, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:179 from nucleotide 751 to nucleotide 906. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:179 from nucleotide 829 to nucleotide 906, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:179 from nucleotide 829 to nucleotide 906, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:179 from nucleotide 829 to nucleotide 906. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:179 from nucleotide 556 to nucleotide 831, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:179 from nucleotide 556 to nucleotide 831, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:179 from nucleotide 556 to nucleotide 831.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:180;

(b) the amino acid sequence of SEQ ID NO:180 from amino acid 1 to amino acid 27;

(c) a fragment of the amino acid sequence of SEQ ID NO:180, the fragment comprising eight contiguous amino acids of SEQ ID NO:180; and

(d) the amino acid sequence encoded by the cDNA insert of clone BN387_3 deposited with the ATCC under accession number 98292;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:180 or the amino acid sequence of SEQ ID NO:180 from amino acid 1 to amino acid 27. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:180 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:180, or a protein

a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:180 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:180, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:180 having biological activity, the fragment comprising the amino acid sequence from amino acid 21 to amino acid 30 of SEQ ID NO:180.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:179.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:179, but excluding the poly(A) tail at the 3' end of SEQ ID NO:179; and

(ab) the nucleotide sequence of the cDNA insert of clone BN387_3 deposited with the ATCC under accession number 98292;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:179, but excluding the poly(A) tail at the 3' end of SEQ ID NO:179; and

(bb) the nucleotide sequence of the cDNA insert of clone BN387_3 deposited with the ATCC under accession number 98292;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BN387_3 deposited with the ATCC under accession number 98292;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BN387_3 deposited with the ATCC under accession number 98292;

(g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BN387_3 deposited with the ATCC under accession number 98292;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BN387_3 deposited with the ATCC under accession number 98292;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:180;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:180 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:180;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:179.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:179 from nucleotide 751 to nucleotide 906; the nucleotide sequence of SEQ ID NO:179 from nucleotide 829 to nucleotide 906; the nucleotide sequence of SEQ ID NO:179 from nucleotide 556 to nucleotide 831; the nucleotide sequence of the full-length protein coding sequence of clone BN387_3 deposited with the ATCC under accession number 98292; or the nucleotide sequence of a mature protein coding sequence of clone BN387_3 deposited with the ATCC under accession number 98292. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BN387_3 deposited with the ATCC under accession number 98292. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:180 from amino acid 1 to amino acid 27. In further preferred embodiments, the present invention provides

polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:177 from nucleotide 928 to nucleotide 1134, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:177 from nucleotide 928 to nucleotide 1134, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:177 from nucleotide 928 to nucleotide 1134.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:178;

(b) the amino acid sequence of SEQ ID NO:178 from amino acid 5 to amino acid 72;

(c) a fragment of the amino acid sequence of SEQ ID NO:178, the fragment comprising eight contiguous amino acids of SEQ ID NO:178; and

(d) the amino acid sequence encoded by the cDNA insert of clone AM666_1 deposited with the ATCC under accession number 98292;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:178 or the amino acid sequence of SEQ ID NO:178 from amino acid 5 to amino acid 72. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:178 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:178, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:178 having biological activity, the fragment comprising the amino acid sequence from amino acid 52 to amino acid 61 of SEQ ID NO:178.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:179;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:179 from nucleotide 751 to nucleotide 906;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:179 from nucleotide 829 to nucleotide 906;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:179 from nucleotide 556 to nucleotide 831;

(aa) SEQ ID NO:177, but excluding the poly(A) tail at the 3' end of SEQ ID NO:177; and

(ab) the nucleotide sequence of the cDNA insert of clone AM666_1 deposited with the ATCC under accession number 98292;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:177, but excluding the poly(A) tail at the 3' end of SEQ ID NO:177; and

(bb) the nucleotide sequence of the cDNA insert of clone AM666_1 deposited with the ATCC under accession number 98292;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:177, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:177 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:177 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:177. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:177 from nucleotide 918 to nucleotide 1262, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:177 from nucleotide 918 to nucleotide 1262, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:177 from nucleotide 918 to nucleotide 1262. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:177 from nucleotide 999 to nucleotide 1262, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:177 from nucleotide 999 to nucleotide 1262, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:177 from nucleotide 999 to nucleotide 1262. Also preferably the

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:177.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:177 from nucleotide 918 to nucleotide 1262; the nucleotide sequence of SEQ ID NO:177 from nucleotide 999 to nucleotide 1262; the nucleotide sequence of SEQ ID NO:177 from nucleotide 928 to nucleotide 1134; the nucleotide sequence of the full-length protein coding sequence of clone AM666_1 deposited with the ATCC under accession number 98292; or the nucleotide sequence of a mature protein coding sequence of clone AM666_1 deposited with the ATCC under accession number 98292. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AM666_1 deposited with the ATCC under accession number 98292. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:178 from amino acid 5 to amino acid 72. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:178 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:178, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:178 having biological activity, the fragment comprising the amino acid sequence from amino acid 52 to amino acid 61 of SEQ ID NO:178.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:177.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(d) the amino acid sequence encoded by the cDNA insert of clone CZ247_2 deposited with the ATCC under accession number 98279;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:176 or the amino acid sequence of SEQ ID NO:176 from amino acid 298 to amino acid 374. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:176 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:176, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:176 having biological activity, the fragment comprising the amino acid sequence from amino acid 276 to amino acid 285 of SEQ ID NO:176.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:177;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:177 from nucleotide 918 to nucleotide 1262;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:177 from nucleotide 999 to nucleotide 1262;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:177 from nucleotide 928 to nucleotide 1134;

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AM666_1 deposited with the ATCC under accession number 98292;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AM666_1 deposited with the ATCC under accession number 98292;

(g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AM666_1 deposited with the ATCC under accession number 98292;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AM666_1 deposited with the ATCC under accession number 98292;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:178;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:178 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:178;

(bb) the nucleotide sequence of the cDNA insert of clone CZ247_2 deposited with the ATCC under accession number 98279;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:175, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:175 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:175 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:175. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:175 from nucleotide 11 to nucleotide 1699, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:175 from nucleotide 11 to nucleotide 1699, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:175 from nucleotide 11 to nucleotide 1699. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:175 from nucleotide 1682 to nucleotide 1699, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:175 from nucleotide 1682 to nucleotide 1699, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:175 from nucleotide 1682 to nucleotide 1699. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:175 from nucleotide 737 to nucleotide 1134, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:175 from nucleotide 737 to nucleotide 1134, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:175 from nucleotide 737 to nucleotide 1134.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:176;

(b) the amino acid sequence of SEQ ID NO:176 from amino acid 298 to amino acid 374;

(c) a fragment of the amino acid sequence of SEQ ID NO:176, the fragment comprising eight contiguous amino acids of SEQ ID NO:176; and

clone CZ247_2 deposited with the ATCC under accession number 98279; or the nucleotide sequence of a mature protein coding sequence of clone CZ247_2 deposited with the ATCC under accession number 98279. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CZ247_2 deposited with the ATCC under accession number 98279. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:176 from amino acid 298 to amino acid 374. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:176 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:176, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:176 having biological activity, the fragment comprising the amino acid sequence from amino acid 276 to amino acid 285 of SEQ ID NO:176.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:175.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:175, but excluding the poly(A) tail at the 3' end of SEQ ID NO:175; and

(ab) the nucleotide sequence of the cDNA insert of clone CZ247_2 deposited with the ATCC under accession number 98279;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:175, but excluding the poly(A) tail at the 3' end of SEQ ID NO:175; and

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:175;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:175 from nucleotide 11 to nucleotide 1699;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:175 from nucleotide 1682 to nucleotide 1699;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:175 from nucleotide 737 to nucleotide 1134;

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CZ247_2 deposited with the ATCC under accession number 98279;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CZ247_2 deposited with the ATCC under accession number 98279;

(g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CZ247_2 deposited with the ATCC under accession number 98279;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CZ247_2 deposited with the ATCC under accession number 98279;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:176;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:176 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:176;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:175.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:175 from nucleotide 11 to nucleotide 1699; the nucleotide sequence of SEQ ID NO:175 from nucleotide 1682 to nucleotide 1699; the nucleotide sequence of SEQ ID NO:175 from nucleotide 737 to nucleotide 1134; the nucleotide sequence of the full-length protein coding sequence of

process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:173 from nucleotide 105 to nucleotide 1007, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:173 from nucleotide 105 to nucleotide 1007, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:173 from nucleotide 105 to nucleotide 1007. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:173 from nucleotide 801 to nucleotide 1007, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:173 from nucleotide 801 to nucleotide 1007, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:173 from nucleotide 801 to nucleotide 1007. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:173 from nucleotide 1 to nucleotide 352, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:173 from nucleotide 1 to nucleotide 352, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:173 from nucleotide 1 to nucleotide 352.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:174;

(b) the amino acid sequence of SEQ ID NO:174 from amino acid 1 to amino acid 83;

(c) a fragment of the amino acid sequence of SEQ ID NO:174, the fragment comprising eight contiguous amino acids of SEQ ID NO:174; and

(d) the amino acid sequence encoded by the cDNA insert of clone CW1155_3 deposited with the ATCC under accession number 98279;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:174 or the amino acid sequence of SEQ ID NO:174 from amino acid 1 to amino acid 83. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:174 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:174, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:174 having biological activity, the fragment comprising the amino acid sequence from amino acid 145 to amino acid 154 of SEQ ID NO:174.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

ID NO:174 having biological activity, the fragment comprising the amino acid sequence from amino acid 145 to amino acid 154 of SEQ ID NO:174.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:173.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:173, but excluding the poly(A) tail at the 3' end of SEQ ID NO:173; and

(ab) the nucleotide sequence of the cDNA insert of clone CW1155_3 deposited with the ATCC under accession number 98279;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:173, but excluding the poly(A) tail at the 3' end of SEQ ID NO:173; and

(bb) the nucleotide sequence of the cDNA insert of clone CW1155_3 deposited with the ATCC under accession number 98279;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:173, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:173 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:173 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:173. Also preferably the polynucleotide isolated according to the above

(g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CW1155_3 deposited with the ATCC under accession number 98279;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CW1155_3 deposited with the ATCC under accession number 98279;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:174;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:174 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:174;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:173.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:173 from nucleotide 105 to nucleotide 1007; the nucleotide sequence of SEQ ID NO:173 from nucleotide 801 to nucleotide 1007; the nucleotide sequence of SEQ ID NO:173 from nucleotide 1 to nucleotide 352; the nucleotide sequence of the full-length protein coding sequence of clone CW1155_3 deposited with the ATCC under accession number 98279; or the nucleotide sequence of a mature protein coding sequence of clone CW1155_3 deposited with the ATCC under accession number 98279. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CW1155_3 deposited with the ATCC under accession number 98279. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:174 from amino acid 1 to amino acid 83. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:174 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:174, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ

from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:171 from nucleotide 265 to nucleotide 515, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:171 from nucleotide 265 to nucleotide 515.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:172;

(b) the amino acid sequence of SEQ ID NO:172 from amino acid 64 to amino acid 138;

(c) a fragment of the amino acid sequence of SEQ ID NO:172, the fragment comprising eight contiguous amino acids of SEQ ID NO:172; and

(d) the amino acid sequence encoded by the cDNA insert of clone CP258_3 deposited with the ATCC under accession number 98279;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:172 or the amino acid sequence of SEQ ID NO:172 from amino acid 64 to amino acid 138. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:172 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:172, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:172 having biological activity, the fragment comprising the amino acid sequence from amino acid 64 to amino acid 73 of SEQ ID NO:172.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:173;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:173 from nucleotide 105 to nucleotide 1007;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:173 from nucleotide 801 to nucleotide 1007;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:173 from nucleotide 1 to nucleotide 352;

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CW1155_3 deposited with the ATCC under accession number 98279;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CW1155_3 deposited with the ATCC under accession number 98279;

(ab) the nucleotide sequence of the cDNA insert of clone CP258_3 deposited with the ATCC under accession number 98279;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:171, but excluding the poly(A) tail at the 3' end of SEQ ID NO:171; and

(bb) the nucleotide sequence of the cDNA insert of clone CP258_3 deposited with the ATCC under accession number 98279;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:171, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:171 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:171 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:171. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:171 from nucleotide 40 to nucleotide 455, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:171 from nucleotide 40 to nucleotide 455, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:171 from nucleotide 40 to nucleotide 455. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:171 from nucleotide 85 to nucleotide 455, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:171 from nucleotide 85 to nucleotide 455, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:171 from nucleotide 85 to nucleotide 455. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:171 from nucleotide 265 to nucleotide 515, and extending contiguously

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:171.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:171 from nucleotide 40 to nucleotide 455; the nucleotide sequence of SEQ ID NO:171 from nucleotide 85 to nucleotide 455; the nucleotide sequence of SEQ ID NO:171 from nucleotide 265 to nucleotide 515; the nucleotide sequence of the full-length protein coding sequence of clone CP258_3 deposited with the ATCC under accession number 98279; or the nucleotide sequence of a mature protein coding sequence of clone CP258_3 deposited with the ATCC under accession number 98279. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CP258_3 deposited with the ATCC under accession number 98279. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:172 from amino acid 64 to amino acid 138. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:172 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:172, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:172 having biological activity, the fragment comprising the amino acid sequence from amino acid 64 to amino acid 73 of SEQ ID NO:172.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:171.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:171, but excluding the poly(A) tail at the 3' end of SEQ ID NO:171; and

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:170 or the amino acid sequence of SEQ ID NO:170 from amino acid 1 to amino acid 44. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:170 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:170, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:170 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID NO:170.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:171;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:171 from nucleotide 40 to nucleotide 455;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:171 from nucleotide 85 to nucleotide 455;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:171 from nucleotide 265 to nucleotide 515;

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CP258_3 deposited with the ATCC under accession number 98279;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CP258_3 deposited with the ATCC under accession number 98279;

(g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CP258_3 deposited with the ATCC under accession number 98279;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CP258_3 deposited with the ATCC under accession number 98279;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:172;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:172 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:172;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:169, but excluding the poly(A) tail at the 3' end of SEQ ID NO:169; and

(bb) the nucleotide sequence of the cDNA insert of clone CO310_2 deposited with the ATCC under accession number 98279;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:169, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:169 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:169 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:169. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:169 from nucleotide 303 to nucleotide 542, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:169 from nucleotide 303 to nucleotide 542, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:169 from nucleotide 303 to nucleotide 542. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:169 from nucleotide 1 to nucleotide 435, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:169 from nucleotide 1 to nucleotide 435, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:169 from nucleotide 1 to nucleotide 435.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:170;

(b) the amino acid sequence of SEQ ID NO:170 from amino acid 1 to amino acid 44;

(c) a fragment of the amino acid sequence of SEQ ID NO:170, the fragment comprising eight contiguous amino acids of SEQ ID NO:170; and

(d) the amino acid sequence encoded by the cDNA insert of clone CO310_2 deposited with the ATCC under accession number 98279;

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:169 from nucleotide 303 to nucleotide 542; the nucleotide sequence of SEQ ID NO:169 from nucleotide 1 to nucleotide 435; the nucleotide sequence of the full-length protein coding sequence of clone CO310_2 deposited with the ATCC under accession number 98279; or the nucleotide sequence of a mature protein coding sequence of clone CO310_2 deposited with the ATCC under accession number 98279. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CO310_2 deposited with the ATCC under accession number 98279. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:170 from amino acid 1 to amino acid 44. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:170 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:170, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:170 having biological activity, the fragment comprising the amino acid sequence from amino acid 34 to amino acid 43 of SEQ ID NO:170.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:169.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:169, but excluding the poly(A) tail at the 3' end of SEQ ID NO:169; and

(ab) the nucleotide sequence of the cDNA insert of clone CO310_2 deposited with the ATCC under accession number 98279;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:168, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:168 having biological activity, the fragment comprising the amino acid sequence from amino acid 52 to amino acid 61 of SEQ ID NO:168.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:169;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:169 from nucleotide 303 to nucleotide 542;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:169 from nucleotide 1 to nucleotide 435;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CO310_2 deposited with the ATCC under accession number 98279;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CO310_2 deposited with the ATCC under accession number 98279;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CO310_2 deposited with the ATCC under accession number 98279;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CO310_2 deposited with the ATCC under accession number 98279;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:170;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:170 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:170;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:169.

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:167, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:167 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:167 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:167. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:167 from nucleotide 176 to nucleotide 520, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:167 from nucleotide 176 to nucleotide 520, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:167 from nucleotide 176 to nucleotide 520. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:167 from nucleotide 317 to nucleotide 520, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:167 from nucleotide 317 to nucleotide 520, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:167 from nucleotide 317 to nucleotide 520. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:167 from nucleotide 118 to nucleotide 413, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:167 from nucleotide 118 to nucleotide 413, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:167 from nucleotide 118 to nucleotide 413.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:168;

(b) the amino acid sequence of SEQ ID NO:168 from amino acid 1 to amino acid 80;

(c) a fragment of the amino acid sequence of SEQ ID NO:168, the fragment comprising eight contiguous amino acids of SEQ ID NO:168; and

(d) the amino acid sequence encoded by the cDNA insert of clone CO223_3 deposited with the ATCC under accession number 98291;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:168 or the amino acid sequence of SEQ ID NO:168 from amino acid 1 to amino acid 80. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:168 having biological activity, the fragment preferably comprising eight (more preferably

polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:168 from amino acid 1 to amino acid 80. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:168 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:168, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:168 having biological activity, the fragment comprising the amino acid sequence from amino acid 52 to amino acid 61 of SEQ ID NO:168.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:167.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:167, but excluding the poly(A) tail at the 3' end of SEQ ID NO:167; and

(ab) the nucleotide sequence of the cDNA insert of clone CO223_3 deposited with the ATCC under accession number 98291;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:167, but excluding the poly(A) tail at the 3' end of SEQ ID NO:167; and

(bb) the nucleotide sequence of the cDNA insert of clone CO223_3 deposited with the ATCC under accession number 98291;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:167 from nucleotide 118 to nucleotide 413;

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CO223_3 deposited with the ATCC under accession number 98291;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CO223_3 deposited with the ATCC under accession number 98291;

(g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CO223_3 deposited with the ATCC under accession number 98291;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CO223_3 deposited with the ATCC under accession number 98291;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:168;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:168 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:168;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:167.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:167 from nucleotide 176 to nucleotide 520; the nucleotide sequence of SEQ ID NO:167 from nucleotide 317 to nucleotide 520; the nucleotide sequence of SEQ ID NO:167 from nucleotide 118 to nucleotide 413; the nucleotide sequence of the full-length protein coding sequence of clone CO223_3 deposited with the ATCC under accession number 98291; or the nucleotide sequence of a mature protein coding sequence of clone CO223_3 deposited with the ATCC under accession number 98291. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CO223_3 deposited with the ATCC under accession number 98291. In yet other preferred embodiments, the present invention provides a

from nucleotide 180 to nucleotide 467, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:164 from nucleotide 180 to nucleotide 467, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:164 from nucleotide 180 to nucleotide 467. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:164 from nucleotide 267 to nucleotide 467, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:164 from nucleotide 267 to nucleotide 467, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:164 from nucleotide 267 to nucleotide 467.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:165;

(b) the amino acid sequence of SEQ ID NO:165 from amino acid 1 to amino acid 37;

(c) a fragment of the amino acid sequence of SEQ ID NO:165, the fragment comprising eight contiguous amino acids of SEQ ID NO:165; and

(d) the amino acid sequence encoded by the cDNA insert of clone CO20_1 deposited with the ATCC under accession number 98279;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:165 or the amino acid sequence of SEQ ID NO:165 from amino acid 1 to amino acid 37. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:165 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:165, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:165 having biological activity, the fragment comprising the amino acid sequence from amino acid 43 to amino acid 52 of SEQ ID NO:165.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:167;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:167 from nucleotide 176 to nucleotide 520;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:167 from nucleotide 317 to nucleotide 520;

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:164;

(ab) SEQ ID NO:166, but excluding the poly(A) tail at the 3' end of SEQ ID NO:166; and

(ac) the nucleotide sequence of the cDNA insert of clone CO20_1 deposited with the ATCC under accession number 98279;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:164;

(bb) SEQ ID NO:166, but excluding the poly(A) tail at the 3' end of SEQ ID NO:166; and

(bc) the nucleotide sequence of the cDNA insert of clone CO20_1 deposited with the ATCC under accession number 98279;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:164 and SEQ ID NO:166, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:164 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:166, but excluding the poly(A) tail at the 3' end of SEQ ID NO:166. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:164, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:164 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:164. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:164

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:165 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:165;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:164.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:164 from nucleotide 180 to nucleotide 467; the nucleotide sequence of SEQ ID NO:164 from nucleotide 267 to nucleotide 467; the nucleotide sequence of the full-length protein coding sequence of clone CO20_1 deposited with the ATCC under accession number 98279; or the nucleotide sequence of a mature protein coding sequence of clone CO20_1 deposited with the ATCC under accession number 98279. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CO20_1 deposited with the ATCC under accession number 98279. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:165 from amino acid 1 to amino acid 37. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:165 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:165, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:165 having biological activity, the fragment comprising the amino acid sequence from amino acid 43 to amino acid 52 of SEQ ID NO:165.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:164 and SEQ ID NO:166.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(a) the amino acid sequence of SEQ ID NO:163;

(b) the amino acid sequence of SEQ ID NO:163 from amino acid 7 to amino acid 48;

(c) a fragment of the amino acid sequence of SEQ ID NO:163, the fragment comprising eight contiguous amino acids of SEQ ID NO:163; and

(d) the amino acid sequence encoded by the cDNA insert of clone CJ160_11 deposited with the ATCC under accession number 98279;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:163 or the amino acid sequence of SEQ ID NO:163 from amino acid 7 to amino acid 48. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:163 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:163, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:163 having biological activity, the fragment comprising the amino acid sequence from amino acid 45 to amino acid 54 of SEQ ID NO:163.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:164;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:164 from nucleotide 180 to nucleotide 467;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:164 from nucleotide 267 to nucleotide 467;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CO20_1 deposited with the ATCC under accession number 98279;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CO20_1 deposited with the ATCC under accession number 98279;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CO20_1 deposited with the ATCC under accession number 98279;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CO20_1 deposited with the ATCC under accession number 98279;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:165;

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:162, but excluding the poly(A) tail at the 3' end of SEQ ID NO:162; and

(bb) the nucleotide sequence of the cDNA insert of clone CJ160_11 deposited with the ATCC under accession number 98279;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:162, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:162 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:162 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:162. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:162 from nucleotide 40 to nucleotide 342, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:162 from nucleotide 40 to nucleotide 342, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:162 from nucleotide 40 to nucleotide 342. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:162 from nucleotide 127 to nucleotide 342, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:162 from nucleotide 127 to nucleotide 342, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:162 from nucleotide 127 to nucleotide 342. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:162 from nucleotide 11 to nucleotide 181, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:162 from nucleotide 11 to nucleotide 181, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:162 from nucleotide 11 to nucleotide 181.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:162.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:162 from nucleotide 40 to nucleotide 342; the nucleotide sequence of SEQ ID NO:162 from nucleotide 127 to nucleotide 342; the nucleotide sequence of SEQ ID NO:162 from nucleotide 11 to nucleotide 181; the nucleotide sequence of the full-length protein coding sequence of clone CJ160_11 deposited with the ATCC under accession number 98279; or the nucleotide sequence of a mature protein coding sequence of clone CJ160_11 deposited with the ATCC under accession number 98279. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CJ160_11 deposited with the ATCC under accession number 98279. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:163 from amino acid 7 to amino acid 48. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:163 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:163, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:163 having biological activity, the fragment comprising the amino acid sequence from amino acid 45 to amino acid 54 of SEQ ID NO:163.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:162.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:162, but excluding the poly(A) tail at the 3' end of SEQ ID NO:162; and

(ab) the nucleotide sequence of the cDNA insert of clone CJ160_11 deposited with the ATCC under accession number 98279;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:161, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:161 having biological activity, the fragment comprising the amino acid sequence from amino acid 482 to amino acid 491 of SEQ ID NO:161.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:162;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:162 from nucleotide 40 to nucleotide 342;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:162 from nucleotide 127 to nucleotide 342;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:162 from nucleotide 11 to nucleotide 181;

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CJ160_11 deposited with the ATCC under accession number 98279;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CJ160_11 deposited with the ATCC under accession number 98279;

(g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CJ160_11 deposited with the ATCC under accession number 98279;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CJ160_11 deposited with the ATCC under accession number 98279;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:163;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:163 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:163;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:160, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:160 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:160 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:160. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO: 160 from nucleotide 126 to nucleotide 3053, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:160 from nucleotide 126 to nucleotide 3053, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:160 from nucleotide 126 to nucleotide 3053. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:160 from nucleotide 180 to nucleotide 3053, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:160 from nucleotide 180 to nucleotide 3053, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:160 from nucleotide 180 to nucleotide 3053. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:160 from nucleotide 49 to nucleotide 382, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:160 from nucleotide 49 to nucleotide 382, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:160 from nucleotide 49 to nucleotide 382.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:161;

(b) the amino acid sequence of SEQ ID NO:161 from amino acid 1 to amino acid 87;

(c) a fragment of the amino acid sequence of SEQ ID NO:161, the fragment comprising eight contiguous amino acids of SEQ ID NO:161; and

(d) the amino acid sequence encoded by the cDNA insert of clone CJ145_1 deposited with the ATCC under accession number 98279;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:161 or the amino acid sequence of SEQ ID NO:161 from amino acid 1 to amino acid 87. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:161 having biological activity, the fragment preferably comprising eight (more preferably

a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:161 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:161, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:161 having biological activity, the fragment comprising the amino acid sequence from amino acid 482 to amino acid 491 of SEQ ID NO:161.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:160.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:160, but excluding the poly(A) tail at the 3' end of SEQ ID NO:160; and

(ab) the nucleotide sequence of the cDNA insert of clone CJ145_1 deposited with the ATCC under accession number 98279;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:160, but excluding the poly(A) tail at the 3' end of SEQ ID NO:160; and

(bb) the nucleotide sequence of the cDNA insert of clone CJ145_1 deposited with the ATCC under accession number 98279;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CJ145_1 deposited with the ATCC under accession number 98279;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CJ145_1 deposited with the ATCC under accession number 98279;

(g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CJ145_1 deposited with the ATCC under accession number 98279;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CJ145_1 deposited with the ATCC under accession number 98279;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:161;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:161 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:161;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:160.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:160 from nucleotide 126 to nucleotide 3053; the nucleotide sequence of SEQ ID NO:160 from nucleotide 180 to nucleotide 3053; the nucleotide sequence of SEQ ID NO:160 from nucleotide 49 to nucleotide 382; the nucleotide sequence of the full-length protein coding sequence of clone CJ145_1 deposited with the ATCC under accession number 98279; or the nucleotide sequence of a mature protein coding sequence of clone CJ145_1 deposited with the ATCC under accession number 98279. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CJ145_1 deposited with the ATCC under accession number 98279. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:161 from amino acid 1 to amino acid 87. In further preferred embodiments, the present invention provides

nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:158 from nucleotide 500 to nucleotide 1108, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:158 from nucleotide 500 to nucleotide 1108. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:158 from nucleotide 1 to nucleotide 387, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:158 from nucleotide 1 to nucleotide 387, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:158 from nucleotide 1 to nucleotide 387.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:159;

(b) the amino acid sequence of SEQ ID NO:159 from amino acid 23 to amino acid 57;

(c) a fragment of the amino acid sequence of SEQ ID NO:159, the fragment comprising eight contiguous amino acids of SEQ ID NO:159; and

(d) the amino acid sequence encoded by the cDNA insert of clone CG300_3 deposited with the ATCC under accession number 98279;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:159 or the amino acid sequence of SEQ ID NO:159 from amino acid 23 to amino acid 57. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:159 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:159, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:159 having biological activity, the fragment comprising the amino acid sequence from amino acid 117 to amino acid 126 of SEQ ID NO:159.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:160;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:160 from nucleotide 126 to nucleotide 3053;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:160 from nucleotide 180 to nucleotide 3053;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:160 from nucleotide 49 to nucleotide 382;

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:158, but excluding the poly(A) tail at the 3' end of SEQ ID NO:158; and

(ab) the nucleotide sequence of the cDNA insert of clone CG300_3 deposited with the ATCC under accession number 98279;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:158, but excluding the poly(A) tail at the 3' end of SEQ ID NO:158; and

(bb) the nucleotide sequence of the cDNA insert of clone CG300_3 deposited with the ATCC under accession number 98279;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:158, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:158 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:158 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:158. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:158 from nucleotide 374 to nucleotide 1108, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:158 from nucleotide 374 to nucleotide 1108, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:158 from nucleotide 374 to nucleotide 1108. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:158 from nucleotide 500 to nucleotide 1108, and extending contiguously from a

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:159 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:159;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:158.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:158 from nucleotide 374 to nucleotide 1108; the nucleotide sequence of SEQ ID NO:158 from nucleotide 500 to nucleotide 1108; the nucleotide sequence of SEQ ID NO:158 from nucleotide 1 to nucleotide 387; the nucleotide sequence of the full-length protein coding sequence of clone CG300_3 deposited with the ATCC under accession number 98279; or the nucleotide sequence of a mature protein coding sequence of clone CG300_3 deposited with the ATCC under accession number 98279. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CG300_3 deposited with the ATCC under accession number 98279. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:159 from amino acid 23 to amino acid 57. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:159 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:159, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:159 having biological activity, the fragment comprising the amino acid sequence from amino acid 117 to amino acid 126 of SEQ ID NO:159.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:158.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(c) a fragment of the amino acid sequence of SEQ ID NO:156, the fragment comprising eight contiguous amino acids of SEQ ID NO:156; and

(d) the amino acid sequence encoded by the cDNA insert of clone CB107_1 deposited with the ATCC under accession number 98279;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:156 or the amino acid sequence of SEQ ID NO:156 from amino acid 127 to amino acid 240. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:156, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological activity, the fragment comprising the amino acid sequence from amino acid 115 to amino acid 124 of SEQ ID NO:156.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:158;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:158 from nucleotide 374 to nucleotide 1108;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:158 from nucleotide 500 to nucleotide 1108;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:158 from nucleotide 1 to nucleotide 387;

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CG300_3 deposited with the ATCC under accession number 98279;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CG300_3 deposited with the ATCC under accession number 98279;

(g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CG300_3 deposited with the ATCC under accession number 98279;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CG300_3 deposited with the ATCC under accession number 98279;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:159;

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:154;

(bb) SEQ ID NO:155;

(bc) SEQ ID NO:157, but excluding the poly(A) tail at the 3' end of SEQ ID NO:157; and

(bd) the nucleotide sequence of the cDNA insert of clone CB107_1 deposited with the ATCC under accession number 98279;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:154, SEQ ID NO:155, and SEQ ID NO:157, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:154 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:157, but excluding the poly(A) tail at the 3' end of SEQ ID NO:157. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:155, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:155 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:155. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:155 from nucleotide 41 to nucleotide 760, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:155 from nucleotide 41 to nucleotide 760, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:155 from nucleotide 41 to nucleotide 760.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:156;

(b) the amino acid sequence of SEQ ID NO:156 from amino acid 127 to amino acid 240;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:155.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:155 from nucleotide 41 to nucleotide 760; the nucleotide sequence of the full-length protein coding sequence of clone CB107_1 deposited with the ATCC under accession number 98279; or the nucleotide sequence of a mature protein coding sequence of clone CB107_1 deposited with the ATCC under accession number 98279. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CB107_1 deposited with the ATCC under accession number 98279. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:156 from amino acid 127 to amino acid 240. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:156, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological activity, the fragment comprising the amino acid sequence from amino acid 115 to amino acid 124 of SEQ ID NO:156.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:155, SEQ ID NO:154, and SEQ ID NO:157 .

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:154;

(ab) SEQ ID NO:155;

(ac) SEQ ID NO:157, but excluding the poly(A) tail at the 3' end of SEQ ID NO:157; and

(ad) the nucleotide sequence of the cDNA insert of clone CB107_1 deposited with the ATCC under accession number 98279;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:153 or the amino acid sequence of SEQ ID NO:153 from amino acid 75 to amino acid 251. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:153 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:153, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:153 having biological activity, the fragment comprising the amino acid sequence from amino acid 450 to amino acid 459 of SEQ ID NO:153.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:155;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:155 from nucleotide 41 to nucleotide 760;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CB107_1 deposited with the ATCC under accession number 98279;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CB107_1 deposited with the ATCC under accession number 98279;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CB107_1 deposited with the ATCC under accession number 98279;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CB107_1 deposited with the ATCC under accession number 98279;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:156;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:156 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:156;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:152, but excluding the poly(A) tail at the 3' end of SEQ ID NO:152; and

(bb) the nucleotide sequence of the cDNA insert of clone CT797_3 deposited with the ATCC under accession number 98278;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:152, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:152 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:152 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:152. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:152 from nucleotide 37 to nucleotide 2766, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:152 from nucleotide 37 to nucleotide 2766, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:152 from nucleotide 37 to nucleotide 2766. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:152 from nucleotide 243 to nucleotide 789, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:152 from nucleotide 243 to nucleotide 789, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:152 from nucleotide 243 to nucleotide 789.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:153;

(b) the amino acid sequence of SEQ ID NO:153 from amino acid 75 to amino acid 251;

(c) a fragment of the amino acid sequence of SEQ ID NO:153, the fragment comprising eight contiguous amino acids of SEQ ID NO:153; and

(d) the amino acid sequence encoded by the cDNA insert of clone CT797_3 deposited with the ATCC under accession number 98278;

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:152 from nucleotide 37 to nucleotide 2766; the nucleotide sequence of SEQ ID NO:152 from nucleotide 243 to nucleotide 789; the nucleotide sequence of the full-length protein coding sequence of clone CT797_3 deposited with the ATCC under accession number 98278; or the nucleotide sequence of a mature protein coding sequence of clone CT797_3 deposited with the ATCC under accession number 98278. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CT797_3 deposited with the ATCC under accession number 98278. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:153 from amino acid 75 to amino acid 251. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:153 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:153, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:153 having biological activity, the fragment comprising the amino acid sequence from amino acid 450 to amino acid 459 of SEQ ID NO:153.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:152.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:152, but excluding the poly(A) tail at the 3' end of SEQ ID NO:152; and

(ab) the nucleotide sequence of the cDNA insert of clone CT797_3 deposited with the ATCC under accession number 98278;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

comprising a fragment of the amino acid sequence of SEQ ID NO:151 having biological activity, the fragment comprising the amino acid sequence from amino acid 138 to amino acid 147 of SEQ ID NO:151.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:152;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:152 from nucleotide 37 to nucleotide 2766;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:152 from nucleotide 243 to nucleotide 789;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CT797_3 deposited with the ATCC under accession number 98278;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CT797_3 deposited with the ATCC under accession number 98278;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CT797_3 deposited with the ATCC under accession number 98278;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CT797_3 deposited with the ATCC under accession number 98278;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:153;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:153 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:153;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:152.

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:150, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:150 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:150 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:150. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:150 from nucleotide 112 to nucleotide 969, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:150 from nucleotide 112 to nucleotide 969, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:150 from nucleotide 112 to nucleotide 969. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:150 from nucleotide 154 to nucleotide 969, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:150 from nucleotide 154 to nucleotide 969, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:150 from nucleotide 154 to nucleotide 969. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:150 from nucleotide 1 to nucleotide 423, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:150 from nucleotide 1 to nucleotide 423, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:150 from nucleotide 1 to nucleotide 423.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:151;

(b) the amino acid sequence of SEQ ID NO:151 from amino acid 1 to amino acid 104;

(c) a fragment of the amino acid sequence of SEQ ID NO:151, the fragment comprising eight contiguous amino acids of SEQ ID NO:151; and

(d) the amino acid sequence encoded by the cDNA insert of clone CT585_1 deposited with the ATCC under accession number 98278;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:151 or the amino acid sequence of SEQ ID NO:151 from amino acid 1 to amino acid 104. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:151 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:151, or a protein

a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:151 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:151, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:151 having biological activity, the fragment comprising the amino acid sequence from amino acid 138 to amino acid 147 of SEQ ID NO:151.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:150.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:150, but excluding the poly(A) tail at the 3' end of SEQ ID NO:150; and

(ab) the nucleotide sequence of the cDNA insert of clone CT585_1 deposited with the ATCC under accession number 98278;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:150, but excluding the poly(A) tail at the 3' end of SEQ ID NO:150; and

(bb) the nucleotide sequence of the cDNA insert of clone CT585_1 deposited with the ATCC under accession number 98278;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CT585_1 deposited with the ATCC under accession number 98278;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CT585_1 deposited with the ATCC under accession number 98278;

(g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CT585_1 deposited with the ATCC under accession number 98278;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CT585_1 deposited with the ATCC under accession number 98278;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:151;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:151 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:151;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:150.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:150 from nucleotide 112 to nucleotide 969; the nucleotide sequence of SEQ ID NO:150 from nucleotide 154 to nucleotide 969; the nucleotide sequence of SEQ ID NO:150 from nucleotide 1 to nucleotide 423; the nucleotide sequence of the full-length protein coding sequence of clone CT585_1 deposited with the ATCC under accession number 98278; or the nucleotide sequence of a mature protein coding sequence of clone CT585_1 deposited with the ATCC under accession number 98278. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CT585_1 deposited with the ATCC under accession number 98278. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:151 from amino acid 1 to amino acid 104. In further preferred embodiments, the present invention provides

corresponding to the 5' end of said sequence of SEQ ID NO:148 from nucleotide 223 to nucleotide 483, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:148 from nucleotide 223 to nucleotide 483. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:148 from nucleotide 22 to nucleotide 397, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:148 from nucleotide 22 to nucleotide 397, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:148 from nucleotide 22 to nucleotide 397.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:149;

(b) the amino acid sequence of SEQ ID NO:149 from amino acid 1 to amino acid 58;

(c) a fragment of the amino acid sequence of SEQ ID NO:149, the fragment comprising eight contiguous amino acids of SEQ ID NO:149; and

(d) the amino acid sequence encoded by the cDNA insert of clone CT550_1 deposited with the ATCC under accession number 98278;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:149 or the amino acid sequence of SEQ ID NO:149 from amino acid 1 to amino acid 58. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:149 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:149, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:149 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:149.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:150;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:150 from nucleotide 112 to nucleotide 969;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:150 from nucleotide 154 to nucleotide 969;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:150 from nucleotide 1 to nucleotide 423;

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:148.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:148, but excluding the poly(A) tail at the 3' end of SEQ ID NO:148; and

(ab) the nucleotide sequence of the cDNA insert of clone CT550_1 deposited with the ATCC under accession number 98278;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:148, but excluding the poly(A) tail at the 3' end of SEQ ID NO:148; and

(bb) the nucleotide sequence of the cDNA insert of clone CT550_1 deposited with the ATCC under accession number 98278;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:148, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:148 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:148 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:148. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:148 from nucleotide 223 to nucleotide 483, and extending contiguously from a nucleotide sequence

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CT550_1 deposited with the ATCC under accession number 98278;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CT550_1 deposited with the ATCC under accession number 98278;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:149;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:149 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:149;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:148.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:148 from nucleotide 223 to nucleotide 483; the nucleotide sequence of SEQ ID NO:148 from nucleotide 22 to nucleotide 397; the nucleotide sequence of the full-length protein coding sequence of clone CT550_1 deposited with the ATCC under accession number 98278; or the nucleotide sequence of a mature protein coding sequence of clone CT550_1 deposited with the ATCC under accession number 98278. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CT550_1 deposited with the ATCC under accession number 98278. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:149 from amino acid 1 to amino acid 58. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:149 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:149, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:149 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:149.

from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:146 from nucleotide 1 to nucleotide 316, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:146 from nucleotide 1 to nucleotide 316.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:147;

(b) the amino acid sequence of SEQ ID NO:147 from amino acid 1 to amino acid 57;

(c) a fragment of the amino acid sequence of SEQ ID NO:147, the fragment comprising eight contiguous amino acids of SEQ ID NO:147; and

(d) the amino acid sequence encoded by the cDNA insert of clone CQ331_2 deposited with the ATCC under accession number 98278;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:147 or the amino acid sequence of SEQ ID NO:147 from amino acid 1 to amino acid 57. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:147 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:147, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:147 having biological activity, the fragment comprising the amino acid sequence from amino acid 129 to amino acid 138 of SEQ ID NO:147.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:148;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:148 from nucleotide 223 to nucleotide 483;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:148 from nucleotide 22 to nucleotide 397;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CT550_1 deposited with the ATCC under accession number 98278;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CT550_1 deposited with the ATCC under accession number 98278;

(ab) the nucleotide sequence of the cDNA insert of clone CQ331_2 deposited with the ATCC under accession number 98278;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:146, but excluding the poly(A) tail at the 3' end of SEQ ID NO:146; and

(bb) the nucleotide sequence of the cDNA insert of clone CQ331_2 deposited with the ATCC under accession number 98278;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:146, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:146 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:146 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:146. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:146 from nucleotide 117 to nucleotide 923, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:146 from nucleotide 117 to nucleotide 923, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:146 from nucleotide 117 to nucleotide 923. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:146 from nucleotide 174 to nucleotide 923, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:146 from nucleotide 174 to nucleotide 923, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:146 from nucleotide 174 to nucleotide 923. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:146 from nucleotide 1 to nucleotide 316, and extending contiguously

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:146.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:146 from nucleotide 117 to nucleotide 923; the nucleotide sequence of SEQ ID NO:146 from nucleotide 174 to nucleotide 923; the nucleotide sequence of SEQ ID NO:146 from nucleotide 1 to nucleotide 316; the nucleotide sequence of the full-length protein coding sequence of clone CQ331_2 deposited with the ATCC under accession number 98278; or the nucleotide sequence of a mature protein coding sequence of clone CQ331_2 deposited with the ATCC under accession number 98278. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CQ331_2 deposited with the ATCC under accession number 98278. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:147 from amino acid 1 to amino acid 57. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:147 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:147, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:147 having biological activity, the fragment comprising the amino acid sequence from amino acid 129 to amino acid 138 of SEQ ID NO:147.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:146.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:146, but excluding the poly(A) tail at the 3' end of SEQ ID NO:146; and

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:145 or the amino acid sequence of SEQ ID NO:145 from amino acid 1 to amino acid 88. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:145 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:145, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:145 having biological activity, the fragment comprising the amino acid sequence from amino acid 149 to amino acid 158 of SEQ ID NO:145.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:146;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:146 from nucleotide 117 to nucleotide 923;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:146 from nucleotide 174 to nucleotide 923;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:146 from nucleotide 1 to nucleotide 316;

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CQ331_2 deposited with the ATCC under accession number 98278;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CQ331_2 deposited with the ATCC under accession number 98278;

(g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CQ331_2 deposited with the ATCC under accession number 98278;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CQ331_2 deposited with the ATCC under accession number 98278;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:147;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:147 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:147;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:144, but excluding the poly(A) tail at the 3' end of SEQ ID NO:144; and

(bb) the nucleotide sequence of the cDNA insert of clone CK201_1 deposited with the ATCC under accession number 98278;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:144, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:144 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:144 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:144. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:144 from nucleotide 189 to nucleotide 1115, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:144 from nucleotide 189 to nucleotide 1115, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:144 from nucleotide 189 to nucleotide 1115. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:144 from nucleotide 1 to nucleotide 451, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:144 from nucleotide 1 to nucleotide 451, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:144 from nucleotide 1 to nucleotide 451.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:145;

(b) the amino acid sequence of SEQ ID NO:145 from amino acid 1 to amino acid 88;

(c) a fragment of the amino acid sequence of SEQ ID NO:145, the fragment comprising eight contiguous amino acids of SEQ ID NO:145; and

(d) the amino acid sequence encoded by the cDNA insert of clone CK201_1 deposited with the ATCC under accession number 98278;

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:144 from nucleotide 189 to nucleotide 1115; the nucleotide sequence of SEQ ID NO:144 from nucleotide 1 to nucleotide 451; the nucleotide sequence of the full-length protein coding sequence of clone CK201_1 deposited with the ATCC under accession number 98278; or the nucleotide sequence of a mature protein coding sequence of clone CK201_1 deposited with the ATCC under accession number 98278. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CK201_1 deposited with the ATCC under accession number 98278. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:145 from amino acid 1 to amino acid 88. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:145 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:145, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:145 having biological activity, the fragment comprising the amino acid sequence from amino acid 149 to amino acid 158 of SEQ ID NO:145.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:144.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:144, but excluding the poly(A) tail at the 3' end of SEQ ID NO:144; and

(ab) the nucleotide sequence of the cDNA insert of clone CK201_1 deposited with the ATCC under accession number 98278;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:143, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:143 having biological activity, the fragment comprising the amino acid sequence from amino acid 26 to amino acid 35 of SEQ ID NO:143.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:144;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:144 from nucleotide 189 to nucleotide 1115;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:144 from nucleotide 1 to nucleotide 451;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CK201_1 deposited with the ATCC under accession number 98278;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CK201_1 deposited with the ATCC under accession number 98278;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CK201_1 deposited with the ATCC under accession number 98278;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CK201_1 deposited with the ATCC under accession number 98278;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:145;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:145 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:145;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:144.

(bb) the nucleotide sequence of the cDNA insert of clone BV291_3 deposited with the ATCC under accession number 98278;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:142, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:142 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:142 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:142. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:142 from nucleotide 1204 to nucleotide 1389, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:142 from nucleotide 1204 to nucleotide 1389, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:142 from nucleotide 1204 to nucleotide 1389. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:142 from nucleotide 881 to nucleotide 1380, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:142 from nucleotide 881 to nucleotide 1380, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:142 from nucleotide 881 to nucleotide 1380.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:143;

(b) the amino acid sequence of SEQ ID NO:143 from amino acid 1 to amino acid 59;

(c) a fragment of the amino acid sequence of SEQ ID NO:143, the fragment comprising eight contiguous amino acids of SEQ ID NO:143; and

(d) the amino acid sequence encoded by the cDNA insert of clone BV291_3 deposited with the ATCC under accession number 98278;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:143 or the amino acid sequence of SEQ ID NO:143 from amino acid 1 to amino acid 59. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:143 having biological activity, the fragment preferably comprising eight (more preferably

nucleotide sequence of a mature protein coding sequence of clone BV291_3 deposited with the ATCC under accession number 98278. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BV291_3 deposited with the ATCC under accession number 98278. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:143 from amino acid 1 to amino acid 59. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:143 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:143, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:143 having biological activity, the fragment comprising the amino acid sequence from amino acid 26 to amino acid 35 of SEQ ID NO:143.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:142.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:142, but excluding the poly(A) tail at the 3' end of SEQ ID NO:142; and

(ab) the nucleotide sequence of the cDNA insert of clone BV291_3 deposited with the ATCC under accession number 98278;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:142, but excluding the poly(A) tail at the 3' end of SEQ ID NO:142; and

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:142;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:142 from nucleotide 1204 to nucleotide 1389;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:142 from nucleotide 881 to nucleotide 1380;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BV291_3 deposited with the ATCC under accession number 98278;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BV291_3 deposited with the ATCC under accession number 98278;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BV291_3 deposited with the ATCC under accession number 98278;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BV291_3 deposited with the ATCC under accession number 98278;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:143;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:143 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:143;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:142.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:142 from nucleotide 1204 to nucleotide 1389; the nucleotide sequence of SEQ ID NO:142 from nucleotide 881 to nucleotide 1380; the nucleotide sequence of the full-length protein coding sequence of clone BV291_3 deposited with the ATCC under accession number 98278; or the

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:140, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:140 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:140 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:140. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:140 from nucleotide 404 to nucleotide 535, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:140 from nucleotide 404 to nucleotide 535, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:140 from nucleotide 404 to nucleotide 535. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:140 from nucleotide 1 to nucleotide 666, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:140 from nucleotide 1 to nucleotide 666, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:140 from nucleotide 1 to nucleotide 666.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:141;

(b) the amino acid sequence of SEQ ID NO:141 from amino acid 1 to amino acid 38;

(c) a fragment of the amino acid sequence of SEQ ID NO:141, the fragment comprising eight contiguous amino acids of SEQ ID NO:141; and

(d) the amino acid sequence encoded by the cDNA insert of clone BV66_1 deposited with the ATCC under accession number 98278;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:141 or the amino acid sequence of SEQ ID NO:141 from amino acid 1 to amino acid 38. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:141 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:141, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:141 having biological activity, the fragment comprising the amino acid sequence from amino acid 17 to amino acid 26 of SEQ ID NO:141.

ATCC under accession number 98278. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:141 from amino acid 1 to amino acid 38. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:141 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:141, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:141 having biological activity, the fragment comprising the amino acid sequence from amino acid 17 to amino acid 26 of SEQ ID NO:141.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:140.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:140, but excluding the poly(A) tail at the 3' end of SEQ ID NO:140; and

(ab) the nucleotide sequence of the cDNA insert of clone BV66_1 deposited with the ATCC under accession number 98278;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:140, but excluding the poly(A) tail at the 3' end of SEQ ID NO:140; and

(bb) the nucleotide sequence of the cDNA insert of clone BV66_1 deposited with the ATCC under accession number 98278;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:140 from nucleotide 404 to nucleotide 535;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:140 from nucleotide 1 to nucleotide 666;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BV66_1 deposited with the ATCC under accession number 98278;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BV66_1 deposited with the ATCC under accession number 98278;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BV66_1 deposited with the ATCC under accession number 98278;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BV66_1 deposited with the ATCC under accession number 98278;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:141;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:141 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:141;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:140.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:140 from nucleotide 404 to nucleotide 535; the nucleotide sequence of SEQ ID NO:140 from nucleotide 1 to nucleotide 666; the nucleotide sequence of the full-length protein coding sequence of clone BV66_1 deposited with the ATCC under accession number 98278; or the nucleotide sequence of a mature protein coding sequence of clone BV66_1 deposited with the ATCC under accession number 98278. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BV66_1 deposited with the

from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:138 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:138 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:138. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:138 from nucleotide 62 to nucleotide 757, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:138 from nucleotide 62 to nucleotide 757, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:138 from nucleotide 62 to nucleotide 757. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:138 from nucleotide 357 to nucleotide 703, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:138 from nucleotide 357 to nucleotide 703, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:138 from nucleotide 357 to nucleotide 703.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:139;

(b) the amino acid sequence of SEQ ID NO:139 from amino acid 184 to amino acid 214;

(c) a fragment of the amino acid sequence of SEQ ID NO:139, the fragment comprising eight contiguous amino acids of SEQ ID NO:139; and

(d) the amino acid sequence encoded by the cDNA insert of clone BG142_1 deposited with the ATCC under accession number 98278;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:139 or the amino acid sequence of SEQ ID NO:139 from amino acid 184 to amino acid 214. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:139 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:139, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:139 having biological activity, the fragment comprising the amino acid sequence from amino acid 111 to amino acid 120 of SEQ ID NO:139.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:140;

fragment of the amino acid sequence of SEQ ID NO:139 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:139, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:139 having biological activity, the fragment comprising the amino acid sequence from amino acid 111 to amino acid 120 of SEQ ID NO:139.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:138.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:138, but excluding the poly(A) tail at the 3' end of SEQ ID NO:138; and

(ab) the nucleotide sequence of the cDNA insert of clone BG142_1 deposited with the ATCC under accession number 98278;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:138, but excluding the poly(A) tail at the 3' end of SEQ ID NO:138; and

(bb) the nucleotide sequence of the cDNA insert of clone BG142_1 deposited with the ATCC under accession number 98278;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:138, and extending contiguously

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BG142_1 deposited with the ATCC under accession number 98278;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BG142_1 deposited with the ATCC under accession number 98278;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BG142_1 deposited with the ATCC under accession number 98278;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BG142_1 deposited with the ATCC under accession number 98278;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:139;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:139 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:139;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:138.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:138 from nucleotide 62 to nucleotide 757; the nucleotide sequence of SEQ ID NO:138 from nucleotide 357 to nucleotide 703; the nucleotide sequence of the full-length protein coding sequence of clone BG142_1 deposited with the ATCC under accession number 98278; or the nucleotide sequence of a mature protein coding sequence of clone BG142_1 deposited with the ATCC under accession number 98278. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BG142_1 deposited with the ATCC under accession number 98278. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:139 from amino acid 184 to amino acid 214. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a

corresponding to the 5' end of said sequence of SEQ ID NO:136 from nucleotide 7 to nucleotide 1647, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:136 from nucleotide 7 to nucleotide 1647. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:136 from nucleotide 1 to nucleotide 305, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:136 from nucleotide 1 to nucleotide 305, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:136 from nucleotide 1 to nucleotide 305.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:137;

(b) the amino acid sequence of SEQ ID NO:137 from amino acid 1 to amino acid 68;

(c) a fragment of the amino acid sequence of SEQ ID NO:137, the fragment comprising eight contiguous amino acids of SEQ ID NO:137; and

(d) the amino acid sequence encoded by the cDNA insert of clone AQ73_3 deposited with the ATCC under accession number 98278;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:137 or the amino acid sequence of SEQ ID NO:137 from amino acid 1 to amino acid 68. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:137 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:137, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:137 having biological activity, the fragment comprising the amino acid sequence from amino acid 268 to amino acid 277 of SEQ ID NO:137.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:138;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:138 from nucleotide 62 to nucleotide 757;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:138 from nucleotide 357 to nucleotide 703;

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:136.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:136, but excluding the poly(A) tail at the 3' end of SEQ ID NO:136; and

(ab) the nucleotide sequence of the cDNA insert of clone AQ73_3 deposited with the ATCC under accession number 98278;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:136, but excluding the poly(A) tail at the 3' end of SEQ ID NO:136; and

(bb) the nucleotide sequence of the cDNA insert of clone AQ73_3 deposited with the ATCC under accession number 98278;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:136, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:136 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:136 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:136. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:136 from nucleotide 7 to nucleotide 1647, and extending contiguously from a nucleotide sequence

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AQ73_3 deposited with the ATCC under accession number 98278;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AQ73_3 deposited with the ATCC under accession number 98278;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:137;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:137 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:137;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:136.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:136 from nucleotide 7 to nucleotide 1647; the nucleotide sequence of SEQ ID NO:136 from nucleotide 1 to nucleotide 305; the nucleotide sequence of the full-length protein coding sequence of clone AQ73_3 deposited with the ATCC under accession number 98278; or the nucleotide sequence of a mature protein coding sequence of clone AQ73_3 deposited with the ATCC under accession number 98278. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AQ73_3 deposited with the ATCC under accession number 98278. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:137 from amino acid 1 to amino acid 68. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:137 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:137, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:137 having biological activity, the fragment comprising the amino acid sequence from amino acid 268 to amino acid 277 of SEQ ID NO:137.

process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:133 from nucleotide 22 to nucleotide 462, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:133 from nucleotide 22 to nucleotide 462, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:133 from nucleotide 22 to nucleotide 462.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:134;

(b) the amino acid sequence of SEQ ID NO:134 from amino acid 52 to amino acid 147;

(c) a fragment of the amino acid sequence of SEQ ID NO:134, the fragment comprising eight contiguous amino acids of SEQ ID NO:134; and

(d) the amino acid sequence encoded by the cDNA insert of clone AJ1_1 deposited with the ATCC under accession number 98278;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:134 or the amino acid sequence of SEQ ID NO:134 from amino acid 52 to amino acid 147. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:134 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:134, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:134 having biological activity, the fragment comprising the amino acid sequence from amino acid 68 to amino acid 77 of SEQ ID NO:134.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:136;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:136 from nucleotide 7 to nucleotide 1647;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:136 from nucleotide 1 to nucleotide 305;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AQ73_3 deposited with the ATCC under accession number 98278;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AQ73_3 deposited with the ATCC under accession number 98278;

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:133;

(ab) SEQ ID NO:135, but excluding the poly(A) tail at the 3' end of SEQ ID NO:135; and

(ac) the nucleotide sequence of the cDNA insert of clone AJ1_1 deposited with the ATCC under accession number 98278;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:133;

(bb) SEQ ID NO:135, but excluding the poly(A) tail at the 3' end of SEQ ID NO:135; and

(bc) the nucleotide sequence of the cDNA insert of clone AJ1_1 deposited with the ATCC under accession number 98278;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:133 and SEQ ID NO:135, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:133 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:135, but excluding the poly(A) tail at the 3' end of SEQ ID NO:135. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:133, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:133 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:133. Also preferably the polynucleotide isolated according to the above

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AJ1_1 deposited with the ATCC under accession number 98278;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:134;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:134 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:134;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:133.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:133 from nucleotide 22 to nucleotide 462; the nucleotide sequence of the full-length protein coding sequence of clone AJ1_1 deposited with the ATCC under accession number 98278; or the nucleotide sequence of a mature protein coding sequence of clone AJ1_1 deposited with the ATCC under accession number 98278. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AJ1_1 deposited with the ATCC under accession number 98278. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:134 from amino acid 52 to amino acid 147. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:134 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:134, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:134 having biological activity, the fragment comprising the amino acid sequence from amino acid 68 to amino acid 77 of SEQ ID NO:134.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:133 and SEQ ID NO:135.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

1260, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:131 from nucleotide 1037 to nucleotide 1260, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:131 from nucleotide 1037 to nucleotide 1260.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:132;

(b) the amino acid sequence of SEQ ID NO:132 from amino acid 22 to amino acid 116;

(c) a fragment of the amino acid sequence of SEQ ID NO:132, the fragment comprising eight contiguous amino acids of SEQ ID NO:132; and

(d) the amino acid sequence encoded by the cDNA insert of clone CT748_2 deposited with the ATCC under accession number 98271;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:132 or the amino acid sequence of SEQ ID NO:132 from amino acid 22 to amino acid 116. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:132 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:132, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:132 having biological activity, the fragment comprising the amino acid sequence from amino acid 234 to amino acid 243 of SEQ ID NO:132.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:133;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:133 from nucleotide 22 to nucleotide 462;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AJ1_1 deposited with the ATCC under accession number 98278;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AJ1_1 deposited with the ATCC under accession number 98278;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AJ1_1 deposited with the ATCC under accession number 98278;

(ab) the nucleotide sequence of the cDNA insert of clone CT748_2 deposited with the ATCC under accession number 98271;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:131, but excluding the poly(A) tail at the 3' end of SEQ ID NO:131; and

(bb) the nucleotide sequence of the cDNA insert of clone CT748_2 deposited with the ATCC under accession number 98271;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:131, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:131 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:131 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:131. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:131 from nucleotide 914 to nucleotide 2353, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:131 from nucleotide 914 to nucleotide 2353, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:131 from nucleotide 914 to nucleotide 2353. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:131 from nucleotide 1793 to nucleotide 2353, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:131 from nucleotide 1793 to nucleotide 2353, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:131 from nucleotide 1793 to nucleotide 2353. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:131 from nucleotide 1037 to nucleotide

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:131.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:131 from nucleotide 914 to nucleotide 2353; the nucleotide sequence of SEQ ID NO:131 from nucleotide 1793 to nucleotide 2353; the nucleotide sequence of SEQ ID NO:131 from nucleotide 1037 to nucleotide 1260; the nucleotide sequence of the full-length protein coding sequence of clone CT748_2 deposited with the ATCC under accession number 98271; or the nucleotide sequence of a mature protein coding sequence of clone CT748_2 deposited with the ATCC under accession number 98271. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CT748_2 deposited with the ATCC under accession number 98271. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:132 from amino acid 22 to amino acid 116. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:132 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:132, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:132 having biological activity, the fragment comprising the amino acid sequence from amino acid 234 to amino acid 243 of SEQ ID NO:132.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:131.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:131, but excluding the poly(A) tail at the 3' end of SEQ ID NO:131; and

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:130 or the amino acid sequence of SEQ ID NO:130 from amino acid 1 to amino acid 34. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:130, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130 having biological activity, the fragment comprising the amino acid sequence from amino acid 591 to amino acid 600 of SEQ ID NO:130.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:131;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:131 from nucleotide 914 to nucleotide 2353;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:131 from nucleotide 1793 to nucleotide 2353;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:131 from nucleotide 1037 to nucleotide 1260;

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CT748_2 deposited with the ATCC under accession number 98271;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CT748_2 deposited with the ATCC under accession number 98271;

(g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CT748_2 deposited with the ATCC under accession number 98271;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CT748_2 deposited with the ATCC under accession number 98271;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:132;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:132 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:132;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:129, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:129 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:129 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:129. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:129 from nucleotide 383 to nucleotide 3958, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:129 from nucleotide 383 to nucleotide 3958, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:129 from nucleotide 383 to nucleotide 3958. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:129 from nucleotide 470 to nucleotide 3958, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:129 from nucleotide 470 to nucleotide 3958, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:129 from nucleotide 470 to nucleotide 3958. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:129 from nucleotide 271 to nucleotide 488, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:129 from nucleotide 271 to nucleotide 488, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:129 from nucleotide 271 to nucleotide 488.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:130;

(b) the amino acid sequence of SEQ ID NO:130 from amino acid 1 to amino acid 34;

(c) a fragment of the amino acid sequence of SEQ ID NO:130, the fragment comprising eight contiguous amino acids of SEQ ID NO:130; and

(d) the amino acid sequence encoded by the cDNA insert of clone CO722_1 deposited with the ATCC under accession number 98271;

mature protein encoded by the cDNA insert of clone CO722_1 deposited with the ATCC under accession number 98271. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:130 from amino acid 1 to amino acid 34. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:130, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130 having biological activity, the fragment comprising the amino acid sequence from amino acid 591 to amino acid 600 of SEQ ID NO:130.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:129.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:129, but excluding the poly(A) tail at the 3' end of SEQ ID NO:129; and

(ab) the nucleotide sequence of the cDNA insert of clone CO722_1 deposited with the ATCC under accession number 98271;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:129, but excluding the poly(A) tail at the 3' end of SEQ ID NO:129; and

(bb) the nucleotide sequence of the cDNA insert of clone CO722_1 deposited with the ATCC under accession number 98271;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:129 from nucleotide 470 to nucleotide 3958;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:129 from nucleotide 271 to nucleotide 488;

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CO722_1 deposited with the ATCC under accession number 98271;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CO722_1 deposited with the ATCC under accession number 98271;

(g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CO722_1 deposited with the ATCC under accession number 98271;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CO722_1 deposited with the ATCC under accession number 98271;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:130;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:130 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:130;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:129.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:129 from nucleotide 383 to nucleotide 3958; the nucleotide sequence of SEQ ID NO:129 from nucleotide 470 to nucleotide 3958; the nucleotide sequence of SEQ ID NO:129 from nucleotide 271 to nucleotide 488; the nucleotide sequence of the full-length protein coding sequence of clone CO722_1 deposited with the ATCC under accession number 98271; or the nucleotide sequence of a mature protein coding sequence of clone CO722_1 deposited with the ATCC under accession number 98271. In other preferred embodiments, the polynucleotide encodes the full-length or a

from nucleotide 128 to nucleotide 1600. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:127 from nucleotide 281 to nucleotide 1600, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:127 from nucleotide 281 to nucleotide 1600, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:127 from nucleotide 281 to nucleotide 1600. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:127 from nucleotide 62 to nucleotide 373, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:127 from nucleotide 62 to nucleotide 373, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:127 from nucleotide 62 to nucleotide 373.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:128;

(b) the amino acid sequence of SEQ ID NO:128 from amino acid 1 to amino acid 82;

(c) a fragment of the amino acid sequence of SEQ ID NO:128, the fragment comprising eight contiguous amino acids of SEQ ID NO:128; and

(d) the amino acid sequence encoded by the cDNA insert of clone CI480_9 deposited with the ATCC under accession number 98271;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:128 or the amino acid sequence of SEQ ID NO:128 from amino acid 1 to amino acid 82. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:128, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128 having biological activity, the fragment comprising the amino acid sequence from amino acid 240 to amino acid 249 of SEQ ID NO:128.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:129;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:129 from nucleotide 383 to nucleotide 3958;

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:127, but excluding the poly(A) tail at the 3' end of SEQ ID NO:127; and

(ab) the nucleotide sequence of the cDNA insert of clone CI480_9 deposited with the ATCC under accession number 98271;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:127, but excluding the poly(A) tail at the 3' end of SEQ ID NO:127; and

(bb) the nucleotide sequence of the cDNA insert of clone CI480_9 deposited with the ATCC under accession number 98271;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:127, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:127 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:127 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:127. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:127 from nucleotide 128 to nucleotide 1600, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:127 from nucleotide 128 to nucleotide 1600, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:127

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CI480_9 deposited with the ATCC under accession number 98271;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:128;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:128;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:127.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:127 from nucleotide 128 to nucleotide 1600; the nucleotide sequence of SEQ ID NO:127 from nucleotide 281 to nucleotide 1600; the nucleotide sequence of SEQ ID NO:127 from nucleotide 62 to nucleotide 373; the nucleotide sequence of the full-length protein coding sequence of clone CI480_9 deposited with the ATCC under accession number 98271; or the nucleotide sequence of a mature protein coding sequence of clone CI480_9 deposited with the ATCC under accession number 98271. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CI480_9 deposited with the ATCC under accession number 98271. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:128 from amino acid 1 to amino acid 82. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128 having biological activity, thc fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:128, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:128 having biological activity, the fragment comprising the amino acid sequence from amino acid 240 to amino acid 249 of SEQ ID NO:128.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:127.

nucleotide 270 to nucleotide 419, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:125 from nucleotide 270 to nucleotide 419.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:126;

(b) a fragment of the amino acid sequence of SEQ ID NO:126, the fragment comprising eight contiguous amino acids of SEQ ID NO:126; and

(c) the amino acid sequence encoded by the cDNA insert of clone CC247_10 deposited with the ATCC under accession number 98271;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:126. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:126 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:126, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:126 having biological activity, the fragment comprising the amino acid sequence from amino acid 7 to amino acid 16 of SEQ ID NO:126.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:127;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:127 from nucleotide 128 to nucleotide 1600;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:127 from nucleotide 281 to nucleotide 1600;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:127 from nucleotide 62 to nucleotide 373;

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CI480_9 deposited with the ATCC under accession number 98271;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CI480_9 deposited with the ATCC under accession number 98271;

(g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CI480_9 deposited with the ATCC under accession number 98271;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:125, but excluding the poly(A) tail at the 3' end of SEQ ID NO:125; and

(bb) the nucleotide sequence of the cDNA insert of clone CC247_10 deposited with the ATCC under accession number 98271;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:125, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:125 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:125 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:125. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:125 from nucleotide 338 to nucleotide 409, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:125 from nucleotide 338 to nucleotide 409, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:125 from nucleotide 338 to nucleotide 409. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:125 from nucleotide 362 to nucleotide 409, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:125 from nucleotide 362 to nucleotide 409, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:125 from nucleotide 362 to nucleotide 409. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:125 from nucleotide 270 to nucleotide 419, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:125 from

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:125.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:125 from nucleotide 338 to nucleotide 409; the nucleotide sequence of SEQ ID NO:125 from nucleotide 362 to nucleotide 409; the nucleotide sequence of SEQ ID NO:125 from nucleotide 270 to nucleotide 419; the nucleotide sequence of the full-length protein coding sequence of clone CC247_10 deposited with the ATCC under accession number 98271; or the nucleotide sequence of a mature protein coding sequence of clone CC247_10 deposited with the ATCC under accession number 98271. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CC247_10 deposited with the ATCC under accession number 98271. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:126 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:126, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:126 having biological activity, the fragment comprising the amino acid sequence from amino acid 7 to amino acid 16 of SEQ ID NO:126.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:125.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:125, but excluding the poly(A) tail at the 3' end of SEQ ID NO:125; and

(ab) the nucleotide sequence of the cDNA insert of clone CC247_10 deposited with the ATCC under accession number 98271;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:124 or the amino acid sequence of SEQ ID NO:124 from amino acid 1 to amino acid 51. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:124 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:124, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:124 having biological activity, the fragment comprising the amino acid sequence from amino acid 26 to amino acid 35 of SEQ ID NO:124.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:125;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:125 from nucleotide 338 to nucleotide 409;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:125 from nucleotide 362 to nucleotide 409;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:125 from nucleotide 270 to nucleotide 419;

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CC247_10 deposited with the ATCC under accession number 98271;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CC247_10 deposited with the ATCC under accession number 98271;

(g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CC247_10 deposited with the ATCC under accession number 98271;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CC247_10 deposited with the ATCC under accession number 98271;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:126;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:126 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:126;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:123, but excluding the poly(A) tail at the 3' end of SEQ ID NO:123; and

(bb) the nucleotide sequence of the cDNA insert of clone BV172_2 deposited with the ATCC under accession number 98271;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:123, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:123 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:123 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:123. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:123 from nucleotide 27 to nucleotide 215, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:123 from nucleotide 27 to nucleotide 215, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:123 from nucleotide 27 to nucleotide 215. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:123 from nucleotide 27 to nucleotide 181, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:123 from nucleotide 27 to nucleotide 181, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:123 from nucleotide 27 to nucleotide 181.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:124;

(b) the amino acid sequence of SEQ ID NO:124 from amino acid 1 to amino acid 51;

(c) a fragment of the amino acid sequence of SEQ ID NO:124, the fragment comprising eight contiguous amino acids of SEQ ID NO:124; and

(d) the amino acid sequence encoded by the cDNA insert of clone BV172_2 deposited with the ATCC under accession number 98271;

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:123 from nucleotide 27 to nucleotide 215; the nucleotide sequence of SEQ ID NO:123 from nucleotide 27 to nucleotide 181; the nucleotide sequence of the full-length protein coding sequence of clone BV172_2 deposited with the ATCC under accession number 98271; or the nucleotide sequence of a mature protein coding sequence of clone BV172_2 deposited with the ATCC under accession number 98271. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BV172_2 deposited with the ATCC under accession number 98271. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:124 from amino acid 1 to amino acid 51. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:124 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:124, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:124 having biological activity, the fragment comprising the amino acid sequence from amino acid 26 to amino acid 35 of SEQ ID NO:124.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:123.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:123, but excluding the poly(A) tail at the 3' end of SEQ ID NO:123; and

(ab) the nucleotide sequence of the cDNA insert of clone BV172_2 deposited with the ATCC under accession number 98271;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

comprising a fragment of the amino acid sequence of SEQ ID NO:122 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:122.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:123;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:123 from nucleotide 27 to nucleotide 215;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:123 from nucleotide 27 to nucleotide 181;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BV172_2 deposited with the ATCC under accession number 98271;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BV172_2 deposited with the ATCC under accession number 98271;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BV172_2 deposited with the ATCC under accession number 98271;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BV172_2 deposited with the ATCC under accession number 98271;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:124;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:124 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:124;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:123.

(ba) SEQ ID NO:121, but excluding the poly(A) tail at the 3' end of SEQ ID NO:121; and

(bb) the nucleotide sequence of the cDNA insert of clone BG366_2 deposited with the ATCC under accession number 98271;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:121, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:121 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:121 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:121. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:121 from nucleotide 2115 to nucleotide 2510, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:121 from nucleotide 2115 to nucleotide 2510, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:121 from nucleotide 2115 to nucleotide 2510. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:121 from nucleotide 1 to nucleotide 324, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:121 from nucleotide 1 to nucleotide 324, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:121 from nucleotide 1 to nucleotide 324.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:122;

(b) a fragment of the amino acid sequence of SEQ ID NO:122, the fragment comprising eight contiguous amino acids of SEQ ID NO:122; and

(c) the amino acid sequence encoded by the cDNA insert of clone BG366_2 deposited with the ATCC under accession number 98271;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:122. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:122 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:122, or a protein

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:121 from nucleotide 2115 to nucleotide 2510; the nucleotide sequence of SEQ ID NO:121 from nucleotide 1 to nucleotide 324; the nucleotide sequence of the full-length protein coding sequence of clone BG366_2 deposited with the ATCC under accession number 98271; or the nucleotide sequence of a mature protein coding sequence of clone BG366_2 deposited with the ATCC under accession number 98271. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BG366_2 deposited with the ATCC under accession number 98271. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:122 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:122, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:122 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:122.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:121.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:121, but excluding the poly(A) tail at the 3' end of SEQ ID NO:121; and

(ab) the nucleotide sequence of the cDNA insert of clone BG366_2 deposited with the ATCC under accession number 98271;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:120, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:120 having biological activity, the fragment comprising the amino acid sequence from amino acid 74 to amino acid 83 of SEQ ID NO:120.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:121;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:121 from nucleotide 2115 to nucleotide 2510;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:121 from nucleotide 1 to nucleotide 324;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BG366_2 deposited with the ATCC under accession number 98271;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BG366_2 deposited with the ATCC under accession number 98271;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BG366_2 deposited with the ATCC under accession number 98271;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BG366_2 deposited with the ATCC under accession number 98271;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:122;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:122 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:122;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:121.

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:119, but excluding the poly(A) tail at the 3' end of SEQ ID NO:119; and

(bb) the nucleotide sequence of the cDNA insert of clone BG219_2 deposited with the ATCC under accession number 98271;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:119, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:119 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:119, but excluding the poly(A) tail at the 3' end of SEQ ID NO:119. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:119 from nucleotide 225 to nucleotide 701, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:119 from nucleotide 225 to nucleotide 701, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:119 from nucleotide 225 to nucleotide 701.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:120;

(b) the amino acid sequence of SEQ ID NO:120 from amino acid 1 to amino acid 97;

(c) a fragment of the amino acid sequence of SEQ ID NO:120, the fragment comprising eight contiguous amino acids of SEQ ID NO:120; and

(d) the amino acid sequence encoded by the cDNA insert of clone BG219_2 deposited with the ATCC under accession number 98271;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:120 or the amino acid sequence of SEQ ID NO:120 from amino acid 1 to amino acid 97. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:120 having biological activity, the fragment preferably comprising eight (more preferably

(I) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:119.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:119 from nucleotide 225 to nucleotide 701; the nucleotide sequence of the full-length protein coding sequence of clone BG219_2 deposited with the ATCC under accession number 98271; or the nucleotide sequence of a mature protein coding sequence of clone BG219_2 deposited with the ATCC under accession number 98271. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BG219_2 deposited with the ATCC under accession number 98271. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:120 from amino acid 1 to amino acid 97. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:120 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:120, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:120 having biological activity, the fragment comprising the amino acid sequence from amino acid 74 to amino acid 83 of SEQ ID NO:120.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:119.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:119, but excluding the poly(A) tail at the 3' end of SEQ ID NO:119; and

(ab) the nucleotide sequence of the cDNA insert of clone BG219_2 deposited with the ATCC under accession number 98271;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:117 or the amino acid sequence of SEQ ID NO:117 from amino acid 119 to amino acid 200. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:117 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:117, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:117 having biological activity, the fragment comprising the amino acid sequence from amino acid 95 to amino acid 104 of SEQ ID NO:117.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:119;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:119 from nucleotide 225 to nucleotide 701;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BG219_2 deposited with the ATCC under accession number 98271;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BG219_2 deposited with the ATCC under accession number 98271;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BG219_2 deposited with the ATCC under accession number 98271;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BG219_2 deposited with the ATCC under accession number 98271;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:120;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:120 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:120;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(bc) the nucleotide sequence of the cDNA insert of clone BG132_1 deposited with the ATCC under accession number 98271;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:116 and SEQ ID NO:118, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:116 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:118, but excluding the poly(A) tail at the 3' end of SEQ ID NO:118. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:116, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:116 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:116. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:116 from nucleotide 2 to nucleotide 601, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:116 from nucleotide 2 to nucleotide 601, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:116 from nucleotide 2 to nucleotide 601. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:116 from nucleotide 401 to nucleotide 601, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:116 from nucleotide 401 to nucleotide 601, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:116 from nucleotide 401 to nucleotide 601.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:117;

(b) the amino acid sequence of SEQ ID NO:117 from amino acid 119 to amino acid 200;

(c) a fragment of the amino acid sequence of SEQ ID NO:117, the fragment comprising eight contiguous amino acids of SEQ ID NO:117; and

(d) the amino acid sequence encoded by the cDNA insert of clone BG132_1 deposited with the ATCC under accession number 98271;

mature protein encoded by the cDNA insert of clone BG132_1 deposited with the ATCC under accession number 98271. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:117 from amino acid 119 to amino acid 200. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:117 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:117, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:117 having biological activity, the fragment comprising the amino acid sequence from amino acid 95 to amino acid 104 of SEQ ID NO:117.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:116 and SEQ ID NO:118.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:116;

(ab) SEQ ID NO:118, but excluding the poly(A) tail at the 3' end of SEQ ID NO:118; and

(ac) the nucleotide sequence of the cDNA insert of clone BG132_1 deposited with the ATCC under accession number 98271;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:116;

(bb) SEQ ID NO:118, but excluding the poly(A) tail at the 3' end of SEQ ID NO:118; and

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:116;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:116 from nucleotide 2 to nucleotide 601;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:116 from nucleotide 401 to nucleotide 601;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BG132_1 deposited with the ATCC under accession number 98271;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BG132_1 deposited with the ATCC under accession number 98271;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BG132_1 deposited with the ATCC under accession number 98271;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BG132_1 deposited with the ATCC under accession number 98271;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:117;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:117 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:117;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:116.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:116 from nucleotide 2 to nucleotide 601; the nucleotide sequence of SEQ ID NO:116 from nucleotide 401 to nucleotide 601; the nucleotide sequence of the full-length protein coding sequence of clone BG132_1 deposited with the ATCC under accession number 98271; or the nucleotide sequence of a mature protein coding sequence of clone BG132_1 deposited with the ATCC under accession number 98271. In other preferred embodiments, the polynucleotide encodes the full-length or a

according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:114, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:114 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:114, but excluding the poly(A) tail at the 3' end of SEQ ID NO:114. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:114 from nucleotide 19 to nucleotide 262, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:114 from nucleotide 19 to nucleotide 262, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:114 from nucleotide 19 to nucleotide 262. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:114 from nucleotide 91 to nucleotide 262, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:114 from nucleotide 91 to nucleotide 262, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:114 from nucleotide 91 to nucleotide 262.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:115;

(b) the amino acid sequence of SEQ ID NO:115 from amino acid 1 to amino acid 66;

(c) a fragment of the amino acid sequence of SEQ ID NO:115, the fragment comprising eight contiguous amino acids of SEQ ID NO:115; and

(d) the amino acid sequence encoded by the cDNA insert of clone AT340_1 deposited with the ATCC under accession number 98271;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:115 or the amino acid sequence of SEQ ID NO:115 from amino acid 1 to amino acid 66. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:115 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:115, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:115 having biological activity, the fragment comprising the amino acid sequence from amino acid 35 to amino acid 44 of SEQ ID NO:115.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:114 and SEQ ID NO:113.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:113;

(ab) SEQ ID NO:114, but excluding the poly(A) tail at the 3' end of SEQ ID NO:114; and

(ac) the nucleotide sequence of the cDNA insert of clone AT340_1 deposited with the ATCC under accession number 98271;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:113;

(bb) SEQ ID NO:114, but excluding the poly(A) tail at the 3' end of SEQ ID NO:114; and

(bc) the nucleotide sequence of the cDNA insert of clone AT340_1 deposited with the ATCC under accession number 98271;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:113 and SEQ ID NO:114, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:113 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:114, but excluding the poly(A) tail at the 3' end of SEQ ID NO:114. Also preferably the polynucleotide isolated

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AT340_1 deposited with the ATCC under accession number 98271;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AT340_1 deposited with the ATCC under accession number 98271;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:115;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:115 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:115;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:114.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:114 from nucleotide 19 to nucleotide 262; the nucleotide sequence of SEQ ID NO:114 from nucleotide 91 to nucleotide 262; the nucleotide sequence of the full-length protein coding sequence of clone AT340_1 deposited with the ATCC under accession number 98271; or the nucleotide sequence of a mature protein coding sequence of clone AT340_1 deposited with the ATCC under accession number 98271. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AT340_1 deposited with the ATCC under accession number 98271. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:115 from amino acid 1 to amino acid 66. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:115 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:115, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:115 having biological activity, the fragment comprising the amino acid sequence from amino acid 35 to amino acid 44 of SEQ ID NO:115.

and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:111 from nucleotide 78 to nucleotide 476, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:111 from nucleotide 78 to nucleotide 476.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:112;

(b) the amino acid sequence of SEQ ID NO:112 from amino acid 1 to amino acid 112;

(c) a fragment of the amino acid sequence of SEQ ID NO:112, the fragment comprising eight contiguous amino acids of SEQ ID NO:112; and

(d) the amino acid sequence encoded by the cDNA insert of clone AM795_4 deposited with the ATCC under accession number 98271;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:112 or the amino acid sequence of SEQ ID NO:112 from amino acid 1 to amino acid 112. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:112, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising the amino acid sequence from amino acid 227 to amino acid 236 of SEQ ID NO:112.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:114;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:114 from nucleotide 19 to nucleotide 262;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:114 from nucleotide 91 to nucleotide 262;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AT340_1 deposited with the ATCC under accession number 98271;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AT340_1 deposited with the ATCC under accession number 98271;

(ab) the nucleotide sequence of the cDNA insert of clone AM795_4 deposited with the ATCC under accession number 98271;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:111, but excluding the poly(A) tail at the 3' end of SEQ ID NO:111; and

(bb) the nucleotide sequence of the cDNA insert of clone AM795_4 deposited with the ATCC under accession number 98271;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:111 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:111 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:111. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111 from nucleotide 141 to nucleotide 1532, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:111 from nucleotide 141 to nucleotide 1532, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:111 from nucleotide 141 to nucleotide 1532. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111 from nucleotide 204 to nucleotide 1532, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:111 from nucleotide 204 to nucleotide 1532, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:111 from nucleotide 204 to nucleotide 1532. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111 from nucleotide 78 to nucleotide 476,

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:111.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:111 from nucleotide 141 to nucleotide 1532; the nucleotide sequence of SEQ ID NO:111 from nucleotide 204 to nucleotide 1532; the nucleotide sequence of SEQ ID NO:111 from nucleotide 78 to nucleotide 476; the nucleotide sequence of the full-length protein coding sequence of clone AM795_4 deposited with the ATCC under accession number 98271; or the nucleotide sequence of a mature protein coding sequence of clone AM795_4 deposited with the ATCC under accession number 98271. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AM795_4 deposited with the ATCC under accession number 98271. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:112 from amino acid 1 to amino acid 112. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:112, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising the amino acid sequence from amino acid 227 to amino acid 236 of SEQ ID NO:112.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:111.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:111, but excluding the poly(A) tail at the 3' end of SEQ ID NO:111; and

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:109. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:109 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:109, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:109 having biological activity, the fragment comprising the amino acid sequence from amino acid 18 to amino acid 27 of SEQ ID NO:109.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111 from nucleotide 141 to nucleotide 1532;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111 from nucleotide 204 to nucleotide 1532;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111 from nucleotide 78 to nucleotide 476;

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AM795_4 deposited with the ATCC under accession number 98271;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AM795_4 deposited with the ATCC under accession number 98271;

(g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AM795_4 deposited with the ATCC under accession number 98271;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AM795_4 deposited with the ATCC under accession number 98271;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:112;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:112;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:107;

(bb) SEQ ID NO:108;

(bc) SEQ ID NO:110, but excluding the poly(A) tail at the 3' end of SEQ ID NO:110; and

(bd) the nucleotide sequence of the cDNA insert of clone CJ397_1 deposited with the ATCC under accession number 98264;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:107, SEQ ID NO:108, and SEQ ID NO:110, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:107 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:110, but excluding the poly(A) tail at the 3' end of SEQ ID NO:110. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:108, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:108 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:108. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:108 from nucleotide 471 to nucleotide 611, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:108 from nucleotide 471 to nucleotide 611, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:108 from nucleotide 471 to nucleotide 611.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:109;

(b) a fragment of the amino acid sequence of SEQ ID NO:109, the fragment comprising eight contiguous amino acids of SEQ ID NO:109; and

(c) the amino acid sequence encoded by the cDNA insert of clone CJ397_1 deposited with the ATCC under accession number 98264;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:108.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:108 from nucleotide 471 to nucleotide 611; the nucleotide sequence of the full-length protein coding sequence of clone CJ397_1 deposited with the ATCC under accession number 98264; or the nucleotide sequence of a mature protein coding sequence of clone CJ397_1 deposited with the ATCC under accession number 98264. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CJ397_1 deposited with the ATCC under accession number 98264. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:109 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:109, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:109 having biological activity, the fragment comprising the amino acid sequence from amino acid 18 to amino acid 27 of SEQ ID NO:109.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:108, SEQ ID NO:107, and SEQ ID NO:110 .

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:107;

(ab) SEQ ID NO:108;

(ac) SEQ ID NO:110, but excluding the poly(A) tail at the 3' end of SEQ ID NO:110; and

(ad) the nucleotide sequence of the cDNA insert of clone CJ397_1 deposited with the ATCC under accession number 98264;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:106. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:106, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising the amino acid sequence from amino acid 11 to amino acid 20 of SEQ ID NO:106.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:108;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:108 from nucleotide 471 to nucleotide 611;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CJ397_1 deposited with the ATCC under accession number 98264;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CJ397_1 deposited with the ATCC under accession number 98264;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CJ397_1 deposited with the ATCC under accession number 98264;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CJ397_1 deposited with the ATCC under accession number 98264;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:109;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:109 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:109;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105; and

(bb) the nucleotide sequence of the cDNA insert of clone CG109_1 deposited with the ATCC under accession number 98264;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:105, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:105 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:105 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:105. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:105 from nucleotide 311 to nucleotide 409, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:105 from nucleotide 311 to nucleotide 409, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:105 from nucleotide 311 to nucleotide 409. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:105 from nucleotide 24 to nucleotide 414, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:105 from nucleotide 24 to nucleotide 414, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:105 from nucleotide 24 to nucleotide 414.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:106;

(b) a fragment of the amino acid sequence of SEQ ID NO:106, the fragment comprising eight contiguous amino acids of SEQ ID NO:106; and

(c) the amino acid sequence encoded by the cDNA insert of clone CG109_1 deposited with the ATCC under accession number 98264;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:105.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:105 from nucleotide 311 to nucleotide 409; the nucleotide sequence of SEQ ID NO:105 from nucleotide 24 to nucleotide 414; the nucleotide sequence of the full-length protein coding sequence of clone CG109_1 deposited with the ATCC under accession number 98264; or the nucleotide sequence of a mature protein coding sequence of clone CG109_1 deposited with the ATCC under accession number 98264. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CG109_1 deposited with the ATCC under accession number 98264. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:106, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising the amino acid sequence from amino acid 11 to amino acid 20 of SEQ ID NO:106.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:105.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105; and

(ab) the nucleotide sequence of the cDNA insert of clone CG109_1 deposited with the ATCC under accession number 98264;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:104 or the amino acid sequence of SEQ ID NO:104 from amino acid 1 to amino acid 60. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:104, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:104.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:105;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:105 from nucleotide 311 to nucleotide 409;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:105 from nucleotide 24 to nucleotide 414;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CG109_1 deposited with the ATCC under accession number 98264;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CG109_1 deposited with the ATCC under accession number 98264;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CG109_1 deposited with the ATCC under accession number 98264;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CG109_1 deposited with the ATCC under accession number 98264;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:106;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:106;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(bb) the nucleotide sequence of the cDNA insert of clone CC182_1 deposited with the ATCC under accession number 98264;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:103, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:103 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:103 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:103. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:103 from nucleotide 405 to nucleotide 662, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:103 from nucleotide 405 to nucleotide 662, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:103 from nucleotide 405 to nucleotide 662. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:103 from nucleotide 519 to nucleotide 662, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:103 from nucleotide 519 to nucleotide 662, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:103 from nucleotide 519 to nucleotide 662. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:103 from nucleotide 1 to nucleotide 584, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:103 from nucleotide 1 to nucleotide 584, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:103 from nucleotide 1 to nucleotide 584.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:104;

(b) the amino acid sequence of SEQ ID NO:104 from amino acid 1 to amino acid 60;

(c) a fragment of the amino acid sequence of SEQ ID NO:104, the fragment comprising eight contiguous amino acids of SEQ ID NO:104; and

(d) the amino acid sequence encoded by the cDNA insert of clone CC182_1 deposited with the ATCC under accession number 98264;

CC182_1 deposited with the ATCC under accession number 98264; or the nucleotide sequence of a mature protein coding sequence of clone CC182_1 deposited with the ATCC under accession number 98264. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CC182_1 deposited with the ATCC under accession number 98264. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:104 from amino acid 1 to amino acid 60. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:104, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:104.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:103.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:103, but excluding the poly(A) tail at the 3' end of SEQ ID NO:103; and

(ab) the nucleotide sequence of the cDNA insert of clone CC182_1 deposited with the ATCC under accession number 98264;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:103, but excluding the poly(A) tail at the 3' end of SEQ ID NO:103; and

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103 from nucleotide 405 to nucleotide 662;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103 from nucleotide 519 to nucleotide 662;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103 from nucleotide 1 to nucleotide 584;

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CC182_1 deposited with the ATCC under accession number 98264;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CC182_1 deposited with the ATCC under accession number 98264;

(g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CC182_1 deposited with the ATCC under accession number 98264;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CC182_1 deposited with the ATCC under accession number 98264;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:104;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:104;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:103.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:103 from nucleotide 405 to nucleotide 662; the nucleotide sequence of SEQ ID NO:103 from nucleotide 519 to nucleotide 662; the nucleotide sequence of SEQ ID NO:103 from nucleotide 1 to nucleotide 584; the nucleotide sequence of the full-length protein coding sequence of clone

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:100 and SEQ ID NO:101, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:100 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:101, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:101 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:101 from nucleotide 72 to nucleotide 569, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:101 from nucleotide 72 to nucleotide 569, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:101 from nucleotide 72 to nucleotide 569.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:102;

(b) the amino acid sequence of SEQ ID NO:102 from amino acid 1 to amino acid 124;

(c) a fragment of the amino acid sequence of SEQ ID NO:102, the fragment comprising eight contiguous amino acids of SEQ ID NO:102; and

(d) the amino acid sequence encoded by the cDNA insert of clone BZ16_3 deposited with the ATCC under accession number 98264;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:102 or the amino acid sequence of SEQ ID NO:102 from amino acid 1 to amino acid 124. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:102, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising the amino acid sequence from amino acid 78 to amino acid 87 of SEQ ID NO:102.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:102, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising the amino acid sequence from amino acid 78 to amino acid 87 of SEQ ID NO:102.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:101 and SEQ ID NO:100.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:100;

(ab) SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101; and

(ac) the nucleotide sequence of the cDNA insert of clone BZ16_3 deposited with the ATCC under accession number 98264;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:100;

(bb) SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101; and

(bc) the nucleotide sequence of the cDNA insert of clone BZ16_3 deposited with the ATCC under accession number 98264;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BZ16_3 deposited with the ATCC under accession number 98264;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BZ16_3 deposited with the ATCC under accession number 98264;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BZ16_3 deposited with the ATCC under accession number 98264;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BZ16_3 deposited with the ATCC under accession number 98264;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:102;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:102;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:101.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:101 from nucleotide 72 to nucleotide 569; the nucleotide sequence of the full-length protein coding sequence of clone BZ16_3 deposited with the ATCC under accession number 98264; or the nucleotide sequence of a mature protein coding sequence of clone BZ16_3 deposited with the ATCC under accession number 98264. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BZ16_3 deposited with the ATCC under accession number 98264. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:102 from amino acid 1 to amino acid 124. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:97 and SEQ ID NO:99, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:97 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:99, but excluding the poly(A) tail at the 3' end of SEQ ID NO:99. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:97 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:97. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97 from nucleotide 16 to nucleotide 492, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:97 from nucleotide 16 to nucleotide 492, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:97 from nucleotide 16 to nucleotide 492.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:98;

(b) a fragment of the amino acid sequence of SEQ ID NO:98, the fragment comprising eight contiguous amino acids of SEQ ID NO:98; and

(c) the amino acid sequence encoded by the cDNA insert of clone BP163_1 deposited with the ATCC under accession number 98264;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:98. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:98, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising the amino acid sequence from amino acid 74 to amino acid 83 of SEQ ID NO:98.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:101;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:101 from nucleotide 72 to nucleotide 569;

deposited with the ATCC under accession number 98264. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:98, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising the amino acid sequence from amino acid 74 to amino acid 83 of SEQ ID NO:98.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:97 and SEQ ID NO:99.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:97;

(ab) SEQ ID NO:99, but excluding the poly(A) tail at the 3' end of SEQ ID NO:99; and

(ac) the nucleotide sequence of the cDNA insert of clone BP163_1 deposited with the ATCC under accession number 98264;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:97;

(bb) SEQ ID NO:99, but excluding the poly(A) tail at the 3' end of SEQ ID NO:99; and

(bc) the nucleotide sequence of the cDNA insert of clone BP163_1 deposited with the ATCC under accession number 98264;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:97;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:97 from nucleotide 16 to nucleotide 492;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BP163_1 deposited with the ATCC under accession number 98264;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BP163_1 deposited with the ATCC under accession number 98264;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BP163_1 deposited with the ATCC under accession number 98264;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BP163_1 deposited with the ATCC under accession number 98264;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:98;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:98;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:97.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:97 from nucleotide 16 to nucleotide 492; the nucleotide sequence of the full-length protein coding sequence of clone BP163_1 deposited with the ATCC under accession number 98264; or the nucleotide sequence of a mature protein coding sequence of clone BP163_1 deposited with the ATCC under accession number 98264. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BP163_1

(bb) the nucleotide sequence of the cDNA insert of clone BK158_1 deposited with the ATCC under accession number 98264;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:95, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:95 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:95 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:95. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:95 from nucleotide 112 to nucleotide 978, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:95 from nucleotide 112 to nucleotide 978, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:95 from nucleotide 112 to nucleotide 978. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:95 from nucleotide 436 to nucleotide 1048, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:95 from nucleotide 436 to nucleotide 1048, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:95 from nucleotide 436 to nucleotide 1048.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:96;

(b) a fragment of the amino acid sequence of SEQ ID NO:96, the fragment comprising eight contiguous amino acids of SEQ ID NO:96; and

(c) the amino acid sequence encoded by the cDNA insert of clone BK158_1 deposited with the ATCC under accession number 98264;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:96. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:96, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising the amino acid sequence from amino acid 139 to amino acid 148 of SEQ ID NO:96.

nucleotide 436 to nucleotide 1048; the nucleotide sequence of the full-length protein coding sequence of clone BK158_1 deposited with the ATCC under accession number 98264; or the nucleotide sequence of a mature protein coding sequence of clone BK158_1 deposited with the ATCC under accession number 98264. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BK158_1 deposited with the ATCC under accession number 98264. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:96, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising the amino acid sequence from amino acid 139 to amino acid 148 of SEQ ID NO:96.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:95.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:95, but excluding the poly(A) tail at the 3' end of SEQ ID NO:95; and

(ab) the nucleotide sequence of the cDNA insert of clone BK158_1 deposited with the ATCC under accession number 98264;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:95, but excluding the poly(A) tail at the 3' end of SEQ ID NO:95; and

fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment comprising the amino acid sequence from amino acid 21 to amino acid 30 of SEQ ID NO:94.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:95;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:95 from nucleotide 112 to nucleotide 978;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:95 from nucleotide 436 to nucleotide 1048;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BK158_1 deposited with the ATCC under accession number 98264;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BK158_1 deposited with the ATCC under accession number 98264;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BK158_1 deposited with the ATCC under accession number 98264;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BK158_1 deposited with the ATCC under accession number 98264;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:96;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:96;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:95.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:95 from nucleotide 112 to nucleotide 978; the nucleotide sequence of SEQ ID NO:95 from

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:93 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:93 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:93. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93 from nucleotide 426 to nucleotide 581, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:93 from nucleotide 426 to nucleotide 581, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:93 from nucleotide 426 to nucleotide 581. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93 from nucleotide 495 to nucleotide 581, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:93 from nucleotide 495 to nucleotide 581, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:93 from nucleotide 495 to nucleotide 581. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93 from nucleotide 354 to nucleotide 503, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:93 from nucleotide 354 to nucleotide 503, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:93 from nucleotide 354 to nucleotide 503.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:94;

(b) the amino acid sequence of SEQ ID NO:94 from amino acid 1 to amino acid 26;

(c) a fragment of the amino acid sequence of SEQ ID NO:94, the fragment comprising eight contiguous amino acids of SEQ ID NO:94; and

(d) the amino acid sequence encoded by the cDNA insert of clone BG102_3 deposited with the ATCC under accession number 98264;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:94 or the amino acid sequence of SEQ ID NO:94 from amino acid 1 to amino acid 26. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:94, or a protein comprising a

a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:94, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment comprising the amino acid sequence from amino acid 21 to amino acid 30 of SEQ ID NO:94.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:93.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:93, but excluding the poly(A) tail at the 3' end of SEQ ID NO:93; and

(ab) the nucleotide sequence of the cDNA insert of clone BG102_3 deposited with the ATCC under accession number 98264;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:93, but excluding the poly(A) tail at the 3' end of SEQ ID NO:93; and

(bb) the nucleotide sequence of the cDNA insert of clone BG102_3 deposited with the ATCC under accession number 98264;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BG102_3 deposited with the ATCC under accession number 98264;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BG102_3 deposited with the ATCC under accession number 98264;

(g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BG102_3 deposited with the ATCC under accession number 98264;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BG102_3 deposited with the ATCC under accession number 98264;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:94;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:94;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:93.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:93 from nucleotide 426 to nucleotide 581; the nucleotide sequence of SEQ ID NO:93 from nucleotide 495 to nucleotide 581; the nucleotide sequence of SEQ ID NO:93 from nucleotide 354 to nucleotide 503; the nucleotide sequence of the full-length protein coding sequence of clone BG102_3 deposited with the ATCC under accession number 98264; or the nucleotide sequence of a mature protein coding sequence of clone BG102_3 deposited with the ATCC under accession number 98264. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BG102_3 deposited with the ATCC under accession number 98264. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:94 from amino acid 1 to amino acid 26. In further preferred embodiments, the present invention provides

to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:92, but excluding the poly(A) tail at the 3' end of SEQ ID NO:92. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:90, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:90 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:90. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:90 from nucleotide 583 to nucleotide 756, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:90 from nucleotide 583 to nucleotide 756, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:90 from nucleotide 583 to nucleotide 756.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:91;

(b) a fragment of the amino acid sequence of SEQ ID NO:91, the fragment comprising eight contiguous amino acids of SEQ ID NO:91; and

(c) the amino acid sequence encoded by the cDNA insert of clone BD441_2 deposited with the ATCC under accession number 98264;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:91. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:91 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:91, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:91 having biological activity, the fragment comprising the amino acid sequence from amino acid 24 to amino acid 33 of SEQ ID NO:91.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:93;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:93 from nucleotide 426 to nucleotide 581;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:93 from nucleotide 495 to nucleotide 581;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:93 from nucleotide 354 to nucleotide 503;

sequence of SEQ ID NO:91 having biological activity, the fragment comprising the amino acid sequence from amino acid 24 to amino acid 33 of SEQ ID NO:91.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:90 and SEQ ID NO:92.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:90;

(ab) SEQ ID NO:92, but excluding the poly(A) tail at the 3' end of SEQ ID NO:92; and

(ac) the nucleotide sequence of the cDNA insert of clone BD441_2 deposited with the ATCC under accession number 98264;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:90;

(bb) SEQ ID NO:92, but excluding the poly(A) tail at the 3' end of SEQ ID NO:92; and

(bc) the nucleotide sequence of the cDNA insert of clone BD441_2 deposited with the ATCC under accession number 98264;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:90 and SEQ ID NO:92, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:90

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BD441_2 deposited with the ATCC under accession number 98264;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BD441_2 deposited with the ATCC under accession number 98264;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BD441_2 deposited with the ATCC under accession number 98264;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BD441_2 deposited with the ATCC under accession number 98264;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:91;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:91 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:91;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:90.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:90 from nucleotide 583 to nucleotide 756; the nucleotide sequence of the full-length protein coding sequence of clone BD441_2 deposited with the ATCC under accession number 98264; or the nucleotide sequence of a mature protein coding sequence of clone BD441_2 deposited with the ATCC under accession number 98264. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BD441_2 deposited with the ATCC under accession number 98264. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:91 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:91, or a polynucleotide encoding a protein comprising a fragment of the amino acid

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:86, SEQ ID NO:87, and SEQ ID NO:89, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:86 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:87, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:87 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:87. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:87 from nucleotide 390 to nucleotide 563, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:87 from nucleotide 390 to nucleotide 563, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:87 from nucleotide 390 to nucleotide 563.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:88;

(b) a fragment of the amino acid sequence of SEQ ID NO:88, the fragment comprising eight contiguous amino acids of SEQ ID NO:88; and

(c) the amino acid sequence encoded by the cDNA insert of clone BD441_1 deposited with the ATCC under accession number 98264;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:88. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:88, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising the amino acid sequence from amino acid 24 to amino acid 33 of SEQ ID NO:88.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:90;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:90 from nucleotide 583 to nucleotide 756;

comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:88, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising the amino acid sequence from amino acid 24 to amino acid 33 of SEQ ID NO:88.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:87, SEQ ID NO:86, and SEQ ID NO:89 .

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:86;

(ab) SEQ ID NO:87;

(ac) SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89; and

(ad) the nucleotide sequence of the cDNA insert of clone BD441_1 deposited with the ATCC under accession number 98264;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:86;

(bb) SEQ ID NO:87;

(bc) SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89; and

(bd) the nucleotide sequence of the cDNA insert of clone BD441_1 deposited with the ATCC under accession number 98264;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87 from nucleotide 390 to nucleotide 563;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BD441_1 deposited with the ATCC under accession number 98264;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BD441_1 deposited with the ATCC under accession number 98264;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BD441_1 deposited with the ATCC under accession number 98264;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BD441_1 deposited with the ATCC under accession number 98264;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:88;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:88;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:87.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:87 from nucleotide 390 to nucleotide 563; the nucleotide sequence of the full-length protein coding sequence of clone BD441_1 deposited with the ATCC under accession number 98264; or the nucleotide sequence of a mature protein coding sequence of clone BD441_1 deposited with the ATCC under accession number 98264. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BD441_1 deposited with the ATCC under accession number 98264. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment preferably

corresponding to the 3' end of SEQ ID NO:84, but excluding the poly(A) tail at the 3' end of SEQ ID NO:84. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:84 from nucleotide 43 to nucleotide 297, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:84 from nucleotide 43 to nucleotide 297, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:84 from nucleotide 43 to nucleotide 297. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:84 from nucleotide 94 to nucleotide 297, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:84 from nucleotide 94 to nucleotide 297, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:84 from nucleotide 94 to nucleotide 297. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:84 from nucleotide 1 to nucleotide 379, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:84 from nucleotide 1 to nucleotide 379, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:84 from nucleotide 1 to nucleotide 379.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:85;

(b) a fragment of the amino acid sequence of SEQ ID NO:85, the fragment comprising eight contiguous amino acids of SEQ ID NO:85; and

(c) the amino acid sequence encoded by the cDNA insert of clone CH377_1 deposited with the ATCC under accession number 98261;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:85. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:85 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:85, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:85 having biological activity, the fragment comprising the amino acid sequence from amino acid 37 to amino acid 46 of SEQ ID NO:85.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87;

twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:85, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:85 having biological activity, the fragment comprising the amino acid sequence from amino acid 37 to amino acid 46 of SEQ ID NO:85.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:84.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:84, but excluding the poly(A) tail at the 3' end of SEQ ID NO:84; and

(ab) the nucleotide sequence of the cDNA insert of clone CH377_1 deposited with the ATCC under accession number 98261;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:84, but excluding the poly(A) tail at the 3' end of SEQ ID NO:84; and

(bb) the nucleotide sequence of the cDNA insert of clone CH377_1 deposited with the ATCC under accession number 98261;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:84, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:84 to a nucleotide sequence

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CH377_1 deposited with the ATCC under accession number 98261;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CH377_1 deposited with the ATCC under accession number 98261;

(g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CH377_1 deposited with the ATCC under accession number 98261;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CH377_1 deposited with the ATCC under accession number 98261;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:85;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:85 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:85;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:84.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:84 from nucleotide 43 to nucleotide 297; the nucleotide sequence of SEQ ID NO:84 from nucleotide 94 to nucleotide 297; the nucleotide sequence of SEQ ID NO:84 from nucleotide 1 to nucleotide 379; the nucleotide sequence of the full-length protein coding sequence of clone CH377_1 deposited with the ATCC under accession number 98261; or the nucleotide sequence of a mature protein coding sequence of clone CH377_1 deposited with the ATCC under accession number 98261. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CH377_1 deposited with the ATCC under accession number 98261. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:85 having biological activity, the fragment preferably comprising eight (more preferably

the 5' end of said sequence of SEQ ID NO:82 from nucleotide 604 to nucleotide 771, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:82 from nucleotide 604 to nucleotide 771. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:82 from nucleotide 1 to nucleotide 684, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:82 from nucleotide 1 to nucleotide 684, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:82 from nucleotide 1 to nucleotide 684.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:83;

(b) the amino acid sequence of SEQ ID NO:83 from amino acid 1 to amino acid 27;

(c) a fragment of the amino acid sequence of SEQ ID NO:83, the fragment comprising eight contiguous amino acids of SEQ ID NO:83; and

(d) the amino acid sequence encoded by the cDNA insert of clone BV123_16 deposited with the ATCC under accession number 98261;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:83 or the amino acid sequence of SEQ ID NO:83 from amino acid 1 to amino acid 27. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:83 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:83, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:83 having biological activity, the fragment comprising the amino acid sequence from amino acid 23 to amino acid 32 of SEQ ID NO:83.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:84;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:84 from nucleotide 43 to nucleotide 297;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:84 from nucleotide 94 to nucleotide 297;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:84 from nucleotide 1 to nucleotide 379;

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:82.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:82, but excluding the poly(A) tail at the 3' end of SEQ ID NO:82; and

(ab) the nucleotide sequence of the cDNA insert of clone BV123_16 deposited with the ATCC under accession number 98261;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:82, but excluding the poly(A) tail at the 3' end of SEQ ID NO:82; and

(bb) the nucleotide sequence of the cDNA insert of clone BV123_16 deposited with the ATCC under accession number 98261;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:82, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:82 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:82 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:82. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:82 from nucleotide 604 to nucleotide 771, and extending contiguously from a nucleotide sequence corresponding to

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BV123_16 deposited with the ATCC under accession number 98261;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BV123_16 deposited with the ATCC under accession number 98261;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:83;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:83 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:83;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:82.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:82 from nucleotide 604 to nucleotide 771; the nucleotide sequence of SEQ ID NO:82 from nucleotide 1 to nucleotide 684; the nucleotide sequence of the full-length protein coding sequence of clone BV123_16 deposited with the ATCC under accession number 98261; or the nucleotide sequence of a mature protein coding sequence of clone BV123_16 deposited with the ATCC under accession number 98261. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BV123_16 deposited with the ATCC under accession number 98261. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:83 from amino acid 1 to amino acid 27. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:83 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:83, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:83 having biological activity, the fragment comprising the amino acid sequence from amino acid 23 to amino acid 32 of SEQ ID NO:83.

SEQ ID NO:79 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:79. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:79 from nucleotide 300 to nucleotide 360, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:79 from nucleotide 300 to nucleotide 360, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:79 from nucleotide 300 to nucleotide 360.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:80;

(b) a fragment of the amino acid sequence of SEQ ID NO:80, the fragment comprising eight contiguous amino acids of SEQ ID NO:80; and

(c) the amino acid sequence encoded by the cDNA insert of clone BL229_22 deposited with the ATCC under accession number 98261;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:80. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:80, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising the amino acid sequence from amino acid 5 to amino acid 14 of SEQ ID NO:80.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:82;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:82 from nucleotide 604 to nucleotide 771;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:82 from nucleotide 1 to nucleotide 684;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BV123_16 deposited with the ATCC under accession number 98261;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BV123_16 deposited with the ATCC under accession number 98261;

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:79;

(ab) SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81; and

(ac) the nucleotide sequence of the cDNA insert of clone BL229_22 deposited with the ATCC under accession number 98261;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:79;

(bb) SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81; and

(bc) the nucleotide sequence of the cDNA insert of clone BL229_22 deposited with the ATCC under accession number 98261;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:79 and SEQ ID NO:81, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:79 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:79, and extending contiguously from a nucleotide sequence corresponding to the 5' end of

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BL229_22 deposited with the ATCC under accession number 98261;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BL229_22 deposited with the ATCC under accession number 98261;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:80;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:80;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:79.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:79 from nucleotide 300 to nucleotide 360; the nucleotide sequence of the full-length protein coding sequence of clone BL229_22 deposited with the ATCC under accession number 98261; or the nucleotide sequence of a mature protein coding sequence of clone BL229_22 deposited with the ATCC under accession number 98261. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BL229_22 deposited with the ATCC under accession number 98261. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:80, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising the amino acid sequence from amino acid 5 to amino acid 14 of SEQ ID NO:80.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:79 and SEQ ID NO:81.

nucleotide 509 to nucleotide 619. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:77 from nucleotide 1 to nucleotide 580, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:77 from nucleotide 1 to nucleotide 580, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:77 from nucleotide 1 to nucleotide 580.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:78;

(b) the amino acid sequence of SEQ ID NO:78 from amino acid 1 to amino acid 24;

(c) a fragment of the amino acid sequence of SEQ ID NO:78, the fragment comprising eight contiguous amino acids of SEQ ID NO:78; and

(d) the amino acid sequence encoded by the cDNA insert of clone BD427_1 deposited with the ATCC under accession number 98261;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:78 or the amino acid sequence of SEQ ID NO:78 from amino acid 1 to amino acid 24. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:78, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising the amino acid sequence from amino acid 13 to amino acid 22 of SEQ ID NO:78.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79 from nucleotide 300 to nucleotide 360;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BL229_22 deposited with the ATCC under accession number 98261;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BL229_22 deposited with the ATCC under accession number 98261;

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77; and

(ab) the nucleotide sequence of the cDNA insert of clone BD427_1 deposited with the ATCC under accession number 98261;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77; and

(bb) the nucleotide sequence of the cDNA insert of clone BD427_1 deposited with the ATCC under accession number 98261;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:77, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:77 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:77 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:77. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:77 from nucleotide 509 to nucleotide 619, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:77 from nucleotide 509 to nucleotide 619, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:77 from

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BD427_1 deposited with the ATCC under accession number 98261;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:78;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:78;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:77.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:77 from nucleotide 509 to nucleotide 619; the nucleotide sequence of SEQ ID NO:77 from nucleotide 1 to nucleotide 580; the nucleotide sequence of the full-length protein coding sequence of clone BD427_1 deposited with the ATCC under accession number 98261; or the nucleotide sequence of a mature protein coding sequence of clone BD427_1 deposited with the ATCC under accession number 98261. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BD427_1 deposited with the ATCC under accession number 98261. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:78 from amino acid 1 to amino acid 24. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:78, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising the amino acid sequence from amino acid 13 to amino acid 22 of SEQ ID NO:78.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:77.

sequence corresponding to the 5' end of said sequence of SEQ ID NO:75 from nucleotide 1 to nucleotide 313, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:75 from nucleotide 1 to nucleotide 313.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:76;

(b) the amino acid sequence of SEQ ID NO:76 from amino acid 1 to amino acid 46;

(c) a fragment of the amino acid sequence of SEQ ID NO:76, the fragment comprising eight contiguous amino acids of SEQ ID NO:76; and

(d) the amino acid sequence encoded by the cDNA insert of clone BD339_1 deposited with the ATCC under accession number 98261;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:76 or the amino acid sequence of SEQ ID NO:76 from amino acid 1 to amino acid 46. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:76, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising the amino acid sequence from amino acid 39 to amino acid 48 of SEQ ID NO:76.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77 from nucleotide 509 to nucleotide 619;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77 from nucleotide 1 to nucleotide 580;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BD427_1 deposited with the ATCC under accession number 98261;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BD427_1 deposited with the ATCC under accession number 98261;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BD427_1 deposited with the ATCC under accession number 98261;

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75; and

(ab) the nucleotide sequence of the cDNA insert of clone BD339_1 deposited with the ATCC under accession number 98261;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75; and

(bb) the nucleotide sequence of the cDNA insert of clone BD339_1 deposited with the ATCC under accession number 98261;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:75 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:75 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:75. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75 from nucleotide 174 to nucleotide 440, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:75 from nucleotide 174 to nucleotide 440, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:75 from nucleotide 174 to nucleotide 440. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75 from nucleotide 1 to nucleotide 313, and extending contiguously from a nucleotide

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:76;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:75.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:75 from nucleotide 174 to nucleotide 440; the nucleotide sequence of SEQ ID NO:75 from nucleotide 1 to nucleotide 313; the nucleotide sequence of the full-length protein coding sequence of clone BD339_1 deposited with the ATCC under accession number 98261; or the nucleotide sequence of a mature protein coding sequence of clone BD339_1 deposited with the ATCC under accession number 98261. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BD339_1 deposited with the ATCC under accession number 98261. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:76 from amino acid 1 to amino acid 46. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:76, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising the amino acid sequence from amino acid 39 to amino acid 48 of SEQ ID NO:76.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:75.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

928, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:72 from nucleotide 815 to nucleotide 928.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:73;

(b) a fragment of the amino acid sequence of SEQ ID NO:73, the fragment comprising eight contiguous amino acids of SEQ ID NO:73; and

(c) the amino acid sequence encoded by the cDNA insert of clone BD176_3 deposited with the ATCC under accession number 98261;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:73. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:73 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:73, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:73 having biological activity, the fragment comprising the amino acid sequence from amino acid 21 to amino acid 30 of SEQ ID NO:73.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75 from nucleotide 174 to nucleotide 440;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75 from nucleotide 1 to nucleotide 313;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BD339_1 deposited with the ATCC under accession number 98261;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BD339_1 deposited with the ATCC under accession number 98261;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BD339_1 deposited with the ATCC under accession number 98261;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BD339_1 deposited with the ATCC under accession number 98261;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:76;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:72;

(bb) SEQ ID NO:74, but excluding the poly(A) tail at the 3' end of SEQ ID NO:74; and

(bc) the nucleotide sequence of the cDNA insert of clone BD176_3 deposited with the ATCC under accession number 98261;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:72 and SEQ ID NO:74, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:72 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:74, but excluding the poly(A) tail at the 3' end of SEQ ID NO:74. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:72, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:72 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:72. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:72 from nucleotide 773 to nucleotide 928, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:72 from nucleotide 773 to nucleotide 928, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:72 from nucleotide 773 to nucleotide 928. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:72 from nucleotide 815 to nucleotide 928, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:72 from nucleotide 815 to nucleotide

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:72.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:72 from nucleotide 773 to nucleotide 928; the nucleotide sequence of SEQ ID NO:72 from nucleotide 815 to nucleotide 928; the nucleotide sequence of the full-length protein coding sequence of clone BD176_3 deposited with the ATCC under accession number 98261; or the nucleotide sequence of a mature protein coding sequence of clone BD176_3 deposited with the ATCC under accession number 98261. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BD176_3 deposited with the ATCC under accession number 98261. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:73 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:73, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:73 having biological activity, the fragment comprising the amino acid sequence from amino acid 21 to amino acid 30 of SEQ ID NO:73.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:72 and SEQ ID NO:74.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:72;

(ab) SEQ ID NO:74, but excluding the poly(A) tail at the 3' end of SEQ ID NO:74; and

(ac) the nucleotide sequence of the cDNA insert of clone BD176_3 deposited with the ATCC under accession number 98261;

(d) the amino acid sequence encoded by the cDNA insert of clone AX8_1 deposited with the ATCC under accession number 98261;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:71 or the amino acid sequence of SEQ ID NO:71 from amino acid 1 to amino acid 44. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:71 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:71, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:71 having biological activity, the fragment comprising the amino acid sequence from amino acid 131 to amino acid 140 of SEQ ID NO:71.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:72;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:72 from nucleotide 773 to nucleotide 928;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:72 from nucleotide 815 to nucleotide 928;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BD176_3 deposited with the ATCC under accession number 98261;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BD176_3 deposited with the ATCC under accession number 98261;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BD176_3 deposited with the ATCC under accession number 98261;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BD176_3 deposited with the ATCC under accession number 98261;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:73;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:73 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:73;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(ba) SEQ ID NO:70, but excluding the poly(A) tail at the 3' end of SEQ ID NO:70; and

(bb) the nucleotide sequence of the cDNA insert of clone AX8_1 deposited with the ATCC under accession number 98261;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:70, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:70 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:70 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:70. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:70 from nucleotide 242 to nucleotide 1060, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:70 from nucleotide 242 to nucleotide 1060, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:70 from nucleotide 242 to nucleotide 1060. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:70 from nucleotide 596 to nucleotide 1060, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:70 from nucleotide 596 to nucleotide 1060, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:70 from nucleotide 596 to nucleotide 1060. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:70 from nucleotide 10 to nucleotide 373, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:70 from nucleotide 10 to nucleotide 373, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:70 from nucleotide 10 to nucleotide 373.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:71;

(b) the amino acid sequence of SEQ ID NO:71 from amino acid 1 to amino acid 44;

(c) a fragment of the amino acid sequence of SEQ ID NO:71, the fragment comprising eight contiguous amino acids of SEQ ID NO:71; and

nucleotide 596 to nucleotide 1060; the nucleotide sequence of SEQ ID NO:70 from nucleotide 10 to nucleotide 373; the nucleotide sequence of the full-length protein coding sequence of clone AX8_1 deposited with the ATCC under accession number 98261; or the nucleotide sequence of a mature protein coding sequence of clone AX8_1 deposited with the ATCC under accession number 98261. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AX8_1 deposited with the ATCC under accession number 98261. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:71 from amino acid 1 to amino acid 44. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:71 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:71, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:71 having biological activity, the fragment comprising the amino acid sequence from amino acid 131 to amino acid 140 of SEQ ID NO:71.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:70.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:70, but excluding the poly(A) tail at the 3' end of SEQ ID NO:70; and

(ab) the nucleotide sequence of the cDNA insert of clone AX8_1 deposited with the ATCC under accession number 98261;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:70;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:70 from nucleotide 242 to nucleotide 1060;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:70 from nucleotide 596 to nucleotide 1060;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:70 from nucleotide 10 to nucleotide 373;

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AX8_1 deposited with the ATCC under accession number 98261;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AX8_1 deposited with the ATCC under accession number 98261;

(g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AX8_1 deposited with the ATCC under accession number 98261;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AX8_1 deposited with the ATCC under accession number 98261;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:71;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:71 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:71;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:70.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:70 from nucleotide 242 to nucleotide 1060; the nucleotide sequence of SEQ ID NO:70 from

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:68, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:68 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:68 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:68. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:68 from nucleotide 76 to nucleotide 1050, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:68 from nucleotide 76 to nucleotide 1050, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:68 from nucleotide 76 to nucleotide 1050. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:68 from nucleotide 331 to nucleotide 567, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:68 from nucleotide 331 to nucleotide 567, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:68 from nucleotide 331 to nucleotide 567.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:69;

(b) the amino acid sequence of SEQ ID NO:69 from amino acid 87 to amino acid 164;

(c) a fragment of the amino acid sequence of SEQ ID NO:69, the fragment comprising eight contiguous amino acids of SEQ ID NO:69; and

(d) the amino acid sequence encoded by the cDNA insert of clone AS164_1 deposited with the ATCC under accession number 98261;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:69 or the amino acid sequence of SEQ ID NO:69 from amino acid 87 to amino acid 164. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:69 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:69, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:69 having biological activity, the fragment comprising the amino acid sequence from amino acid 157 to amino acid 166 of SEQ ID NO:69.

deposited with the ATCC under accession number 98261. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:69 from amino acid 87 to amino acid 164. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:69 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:69, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:69 having biological activity, the fragment comprising the amino acid sequence from amino acid 157 to amino acid 166 of SEQ ID NO:69.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:68.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:68, but excluding the poly(A) tail at the 3' end of SEQ ID NO:68; and

(ab) the nucleotide sequence of the cDNA insert of clone AS164_1 deposited with the ATCC under accession number 98261;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:68, but excluding the poly(A) tail at the 3' end of SEQ ID NO:68; and

(bb) the nucleotide sequence of the cDNA insert of clone AS164_1 deposited with the ATCC under accession number 98261;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:68 from nucleotide 76 to nucleotide 1050;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:68 from nucleotide 331 to nucleotide 567;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AS164_1 deposited with the ATCC under accession number 98261;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AS164_1 deposited with the ATCC under accession number 98261;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AS164_1 deposited with the ATCC under accession number 98261;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AS164_1 deposited with the ATCC under accession number 98261;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:69;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:69 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:69;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:68.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:68 from nucleotide 76 to nucleotide 1050; the nucleotide sequence of SEQ ID NO:68 from nucleotide 331 to nucleotide 567; the nucleotide sequence of the full-length protein coding sequence of clone AS164_1 deposited with the ATCC under accession number 98261; or the nucleotide sequence of a mature protein coding sequence of clone AS164_1 deposited with the ATCC under accession number 98261. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AS164_1

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:65 and SEQ ID NO:66, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:65 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:66, but excluding the poly(A) tail at the 3' end of SEQ ID NO:66. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:66, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:66 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:66, but excluding the poly(A) tail at the 3' end of SEQ ID NO:66. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:66 from nucleotide 289 to nucleotide 780, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:66 from nucleotide 289 to nucleotide 780, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:66 from nucleotide 289 to nucleotide 780.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:67;

(b) the amino acid sequence of SEQ ID NO:67 from amino acid 1 to amino acid 160;

(c) a fragment of the amino acid sequence of SEQ ID NO:67, the fragment comprising eight contiguous amino acids of SEQ ID NO:67; and

(d) the amino acid sequence encoded by the cDNA insert of clone AR440_1 deposited with the ATCC under accession number 98261;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:67 or the amino acid sequence of SEQ ID NO:67 from amino acid 1 to amino acid 160. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:67 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:67, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:67 having biological activity, the fragment comprising the amino acid sequence from amino acid 77 to amino acid 86 of SEQ ID NO:67.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:68;

preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:67, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:67 having biological activity, the fragment comprising the amino acid sequence from amino acid 77 to amino acid 86 of SEQ ID NO:67.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:66 and SEQ ID NO:65.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:65;

(ab) SEQ ID NO:66, but excluding the poly(A) tail at the 3' end of SEQ ID NO:66; and

(ac) the nucleotide sequence of the cDNA insert of clone AR440_1 deposited with the ATCC under accession number 98261;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:65;

(bb) SEQ ID NO:66, but excluding the poly(A) tail at the 3' end of SEQ ID NO:66; and

(bc) the nucleotide sequence of the cDNA insert of clone AR440_1 deposited with the ATCC under accession number 98261;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AR440_1 deposited with the ATCC under accession number 98261;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AR440_1 deposited with the ATCC under accession number 98261;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AR440_1 deposited with the ATCC under accession number 98261;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AR440_1 deposited with the ATCC under accession number 98261;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:67;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:67 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:67;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:66.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:66 from nucleotide 289 to nucleotide 780; the nucleotide sequence of the full-length protein coding sequence of clone AR440_1 deposited with the ATCC under accession number 98261; or the nucleotide sequence of a mature protein coding sequence of clone AR440_1 deposited with the ATCC under accession number 98261. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AR440_1 deposited with the ATCC under accession number 98261. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:67 from amino acid 1 to amino acid 160. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:67 having biological activity, the fragment

above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:62, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:62 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:62. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:62 from nucleotide 68 to nucleotide 430, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:62 from nucleotide 68 to nucleotide 430, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:62 from nucleotide 68 to nucleotide 430. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:62 from nucleotide 128 to nucleotide 430, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:62 from nucleotide 128 to nucleotide 430, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:62 from nucleotide 128 to nucleotide 430.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:63;

(b) a fragment of the amino acid sequence of SEQ ID NO:63, the fragment comprising eight contiguous amino acids of SEQ ID NO:63; and

(c) the amino acid sequence encoded by the cDNA insert of clone AJ20_2 deposited with the ATCC under accession number 98261;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:63. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:63 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:63, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:63 having biological activity, the fragment comprising the amino acid sequence from amino acid 55 to amino acid 64 of SEQ ID NO:63.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:66;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:66 from nucleotide 289 to nucleotide 780;

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:62 and SEQ ID NO:64.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:62;

(ab) SEQ ID NO:64, but excluding the poly(A) tail at the 3' end of SEQ ID NO:64; and

(ac) the nucleotide sequence of the cDNA insert of clone AJ20_2 deposited with the ATCC under accession number 98261;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:62;

(bb) SEQ ID NO:64, but excluding the poly(A) tail at the 3' end of SEQ ID NO:64; and

(bc) the nucleotide sequence of the cDNA insert of clone AJ20_2 deposited with the ATCC under accession number 98261;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:62 and SEQ ID NO:64, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:62 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:64, but excluding the poly(A) tail at the 3' end of SEQ ID NO:64. Also preferably the polynucleotide isolated according to the

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AJ20_2 deposited with the ATCC under accession number 98261;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AJ20_2 deposited with the ATCC under accession number 98261;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AJ20_2 deposited with the ATCC under accession number 98261;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:63;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:63 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:63;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:62.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:62 from nucleotide 68 to nucleotide 430; the nucleotide sequence of SEQ ID NO:62 from nucleotide 128 to nucleotide 430; the nucleotide sequence of the full-length protein coding sequence of clone AJ20_2 deposited with the ATCC under accession number 98261; or the nucleotide sequence of a mature protein coding sequence of clone AJ20_2 deposited with the ATCC under accession number 98261. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AJ20_2 deposited with the ATCC under accession number 98261. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:63 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:63, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:63 having biological activity, the fragment comprising the amino acid sequence from amino acid 55 to amino acid 64 of SEQ ID NO:63.

nucleotide 87 to nucleotide 1871. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:60 from nucleotide 628 to nucleotide 1882, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:60 from nucleotide 628 to nucleotide 1882, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:60 from nucleotide 628 to nucleotide 1882.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:61;

(b) the amino acid sequence of SEQ ID NO:61 from amino acid 182 to amino acid 248;

(c) a fragment of the amino acid sequence of SEQ ID NO:61, the fragment comprising eight contiguous amino acids of SEQ ID NO:61; and

(d) the amino acid sequence encoded by the cDNA insert of clone CO390_1 deposited with the ATCC under accession number 98232;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:61 or the amino acid sequence of SEQ ID NO:61 from amino acid 182 to amino acid 248. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:61 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:61, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:61 having biological activity, the fragment comprising the amino acid sequence from amino acid 292 to amino acid 301 of SEQ ID NO:61.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:62;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:62 from nucleotide 68 to nucleotide 430;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:62 from nucleotide 128 to nucleotide 430;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AJ20_2 deposited with the ATCC under accession number 98261;

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:60, but excluding the poly(A) tail at the 3' end of SEQ ID NO:60; and

(ab) the nucleotide sequence of the cDNA insert of clone CO390_1 deposited with the ATCC under accession number 98232;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:60, but excluding the poly(A) tail at the 3' end of SEQ ID NO:60; and

(bb) the nucleotide sequence of the cDNA insert of clone CO390_1 deposited with the ATCC under accession number 98232;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:60, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:60 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:60, but excluding the poly(A) tail at the 3' end of SEQ ID NO:60. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:60 from nucleotide 87 to nucleotide 1871, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:60 from nucleotide 87 to nucleotide 1871, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:60 from

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CO390_1 deposited with the ATCC under accession number 98232;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:61;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:61 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:61;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:60.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:60 from nucleotide 87 to nucleotide 1871; the nucleotide sequence of SEQ ID NO:60 from nucleotide 628 to nucleotide 1882; the nucleotide sequence of the full-length protein coding sequence of clone CO390_1 deposited with the ATCC under accession number 98232; or the nucleotide sequence of a mature protein coding sequence of clone CO390_1 deposited with the ATCC under accession number 98232. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CO390_1 deposited with the ATCC under accession number 98232. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:61 from amino acid 182 to amino acid 248. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:61 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:61, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:61 having biological activity, the fragment comprising the amino acid sequence from amino acid 292 to amino acid 301 of SEQ ID NO:61.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:60.

sequence corresponding to the 5' end of said sequence of SEQ ID NO:58 from nucleotide 868 to nucleotide 1887, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:58 from nucleotide 868 to nucleotide 1887.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:59;

(b) the amino acid sequence of SEQ ID NO:59 from amino acid 1 to amino acid 109;

(c) a fragment of the amino acid sequence of SEQ ID NO:59, the fragment comprising eight contiguous amino acids of SEQ ID NO:59; and

(d) the amino acid sequence encoded by the cDNA insert of clone CN238_1 deposited with the ATCC under accession number 98232;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:59 or the amino acid sequence of SEQ ID NO:59 from amino acid 1 to amino acid 109. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:59 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:59, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:59 having biological activity, the fragment comprising the amino acid sequence from amino acid 65 to amino acid 74 of SEQ ID NO:59.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:60;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:60 from nucleotide 87 to nucleotide 1871;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:60 from nucleotide 628 to nucleotide 1882;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CO390_1 deposited with the ATCC under accession number 98232;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CO390_1 deposited with the ATCC under accession number 98232;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CO390_1 deposited with the ATCC under accession number 98232;

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:58, but excluding the poly(A) tail at the 3' end of SEQ ID NO:58; and

(ab) the nucleotide sequence of the cDNA insert of clone CN238_1 deposited with the ATCC under accession number 98232;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:58, but excluding the poly(A) tail at the 3' end of SEQ ID NO:58; and

(bb) the nucleotide sequence of the cDNA insert of clone CN238_1 deposited with the ATCC under accession number 98232;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:58, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:58 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:58 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:58. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:58 from nucleotide 288 to nucleotide 710, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:58 from nucleotide 288 to nucleotide 710, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:58 from nucleotide 288 to nucleotide 710. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:58 from nucleotide 868 to nucleotide 1887, and extending contiguously from a nucleotide

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:59 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:59;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:58.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:58 from nucleotide 288 to nucleotide 710; the nucleotide sequence of SEQ ID NO:58 from nucleotide 868 to nucleotide 1887; the nucleotide sequence of the full-length protein coding sequence of clone CN238_1 deposited with the ATCC under accession number 98232; or the nucleotide sequence of a mature protein coding sequence of clone CN238_1 deposited with the ATCC under accession number 98232. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CN238_1 deposited with the ATCC under accession number 98232. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:59 from amino acid 1 to amino acid 109. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:59 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:59, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:59 having biological activity, the fragment comprising the amino acid sequence from amino acid 65 to amino acid 74 of SEQ ID NO:59.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:58.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

624, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:55 from nucleotide 325 to nucleotide 624.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:56;

(b) a fragment of the amino acid sequence of SEQ ID NO:56, the fragment comprising eight contiguous amino acids of SEQ ID NO:56; and

(c) the amino acid sequence encoded by the cDNA insert of clone CI522_1 deposited with the ATCC under accession number 98232;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:56. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:56, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID NO:56.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:58;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:58 from nucleotide 288 to nucleotide 710;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:58 from nucleotide 868 to nucleotide 1887;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CN238_1 deposited with the ATCC under accession number 98232;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CN238_1 deposited with the ATCC under accession number 98232;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CN238_1 deposited with the ATCC under accession number 98232;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CN238_1 deposited with the ATCC under accession number 98232;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:59;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:55;

(bb) SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57; and

(bc) the nucleotide sequence of the cDNA insert of clone CI522_1 deposited with the ATCC under accession number 98232;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:55 and SEQ ID NO:57, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:55 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:55 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:55. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55 from nucleotide 268 to nucleotide 624, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:55 from nucleotide 268 to nucleotide 624, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:55 from nucleotide 268 to nucleotide 624. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55 from nucleotide 325 to nucleotide 624, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:55 from nucleotide 325 to nucleotide

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:55.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:55 from nucleotide 268 to nucleotide 624; the nucleotide sequence of SEQ ID NO:55 from nucleotide 325 to nucleotide 624; the nucleotide sequence of the full-length protein coding sequence of clone CI522_1 deposited with the ATCC under accession number 98232; or the nucleotide sequence of a mature protein coding sequence of clone CI522_1 deposited with the ATCC under accession number 98232. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CI522_1 deposited with the ATCC under accession number 98232. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:56, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID NO:56.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:55 and SEQ ID NO:57.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:55;

(ab) SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57; and

(ac) the nucleotide sequence of the cDNA insert of clone CI522_1 deposited with the ATCC under accession number 98232;

(d) the amino acid sequence encoded by the cDNA insert of clone CI490_2 deposited with the ATCC under accession number 98232;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:54 or the amino acid sequence of SEQ ID NO:54 from amino acid 133 to amino acid 270. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:54, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising the amino acid sequence from amino acid 130 to amino acid 139 of SEQ ID NO:54.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55 from nucleotide 268 to nucleotide 624;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55 from nucleotide 325 to nucleotide 624;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CI522_1 deposited with the ATCC under accession number 98232;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CI522_1 deposited with the ATCC under accession number 98232;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CI522_1 deposited with the ATCC under accession number 98232;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CI522_1 deposited with the ATCC under accession number 98232;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:56;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:56;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(ba) SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53; and

(bb) the nucleotide sequence of the cDNA insert of clone CI490_2 deposited with the ATCC under accession number 98232;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:53 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:53 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:53. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53 from nucleotide 232 to nucleotide 1041, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:53 from nucleotide 232 to nucleotide 1041, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide 232 to nucleotide 1041. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53 from nucleotide 460 to nucleotide 1041, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:53 from nucleotide 460 to nucleotide 1041, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide 460 to nucleotide 1041. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53 from nucleotide 590 to nucleotide 1163, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:53 from nucleotide 590 to nucleotide 1163, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide 590 to nucleotide 1163.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:54;

(b) the amino acid sequence of SEQ ID NO:54 from amino acid 133 to amino acid 270;

(c) a fragment of the amino acid sequence of SEQ ID NO:54, the fragment comprising eight contiguous amino acids of SEQ ID NO:54; and

nucleotide 460 to nucleotide 1041; the nucleotide sequence of SEQ ID NO:53 from nucleotide 590 to nucleotide 1163; the nucleotide sequence of the full-length protein coding sequence of clone CI490_2 deposited with the ATCC under accession number 98232; or the nucleotide sequence of a mature protein coding sequence of clone CI490_2 deposited with the ATCC under accession number 98232. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CI490_2 deposited with the ATCC under accession number 98232. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:54 from amino acid 133 to amino acid 270. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:54, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising the amino acid sequence from amino acid 130 to amino acid 139 of SEQ ID NO:54.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:53.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53; and

(ab) the nucleotide sequence of the cDNA insert of clone CI490_2 deposited with the ATCC under accession number 98232;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53 from nucleotide 232 to nucleotide 1041;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53 from nucleotide 460 to nucleotide 1041;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53 from nucleotide 590 to nucleotide 1163;

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CI490_2 deposited with the ATCC under accession number 98232;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CI490_2 deposited with the ATCC under accession number 98232;

(g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CI490_2 deposited with the ATCC under accession number 98232;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CI490_2 deposited with the ATCC under accession number 98232;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:54;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:54;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:53.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:53 from nucleotide 232 to nucleotide 1041; the nucleotide sequence of SEQ ID NO:53 from

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:50 and SEQ ID NO:52, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:50 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:52, but excluding the poly(A) tail at the 3' end of SEQ ID NO:52. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:50, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:50 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:50. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:50 from nucleotide 144 to nucleotide 566, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:50 from nucleotide 144 to nucleotide 566, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:50 from nucleotide 144 to nucleotide 566.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:51;

(b) the amino acid sequence of SEQ ID NO:51 from amino acid 39 to amino acid 141;

(c) a fragment of the amino acid sequence of SEQ ID NO:51, the fragment comprising eight contiguous amino acids of SEQ ID NO:51; and

(d) the amino acid sequence encoded by the cDNA insert of clone BR595_4 deposited with the ATCC under accession number 98232;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:51 or the amino acid sequence of SEQ ID NO:51 from amino acid 39 to amino acid 141. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:51 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:51, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:51 having biological activity, the fragment comprising the amino acid sequence from amino acid 65 to amino acid 74 of SEQ ID NO:51.

deposited with the ATCC under accession number 98232. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:51 from amino acid 39 to amino acid 141. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:51 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:51, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:51 having biological activity, the fragment comprising the amino acid sequence from amino acid 65 to amino acid 74 of SEQ ID NO:51.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:50 and SEQ ID NO:52.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:50;

(ab) SEQ ID NO:52, but excluding the poly(A) tail at the 3' end of SEQ ID NO:52; and

(ac) the nucleotide sequence of the cDNA insert of clone BR595_4 deposited with the ATCC under accession number 98232;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:50;

(bb) SEQ ID NO:52, but excluding the poly(A) tail at the 3' end of SEQ ID NO:52; and

(bc) the nucleotide sequence of the cDNA insert of clone BR595_4 deposited with the ATCC under accession number 98232;

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:50;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:50 from nucleotide 144 to nucleotide 566;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BR595_4 deposited with the ATCC under accession number 98232;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BR595_4 deposited with the ATCC under accession number 98232;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BR595_4 deposited with the ATCC under accession number 98232;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BR595_4 deposited with the ATCC under accession number 98232;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:51;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:51 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:51;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:50.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:50 from nucleotide 144 to nucleotide 566; the nucleotide sequence of the full-length protein coding sequence of clone BR595_4 deposited with the ATCC under accession number 98232; or the nucleotide sequence of a mature protein coding sequence of clone BR595_4 deposited with the ATCC under accession number 98232. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BR595_4

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:47 and SEQ ID NO:49, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:47 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:47 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:47. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47 from nucleotide 45 to nucleotide 428, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:47 from nucleotide 45 to nucleotide 428, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:47 from nucleotide 45 to nucleotide 428.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:48;

(b) the amino acid sequence of SEQ ID NO:48 from amino acid 52 to amino acid 128;

(c) a fragment of the amino acid sequence of SEQ ID NO:48, the fragment comprising eight contiguous amino acids of SEQ ID NO:48; and

(d) the amino acid sequence encoded by the cDNA insert of clone BO538_2 deposited with the ATCC under accession number 98232;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:48 or the amino acid sequence of SEQ ID NO:48 from amino acid 52 to amino acid 128. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:48, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising the amino acid sequence from amino acid 59 to amino acid 68 of SEQ ID NO:48.

deposited with the ATCC under accession number 98232. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:48 from amino acid 52 to amino acid 128. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:48, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising the amino acid sequence from amino acid 59 to amino acid 68 of SEQ ID NO:48.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:47 and SEQ ID NO:49.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:47;

(ab) SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49; and

(ac) the nucleotide sequence of the cDNA insert of clone BO538_2 deposited with the ATCC under accession number 98232;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:47;

(bb) SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49; and

(bc) the nucleotide sequence of the cDNA insert of clone BO538_2 deposited with the ATCC under accession number 98232;

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47 from nucleotide 45 to nucleotide 428;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BO538_2 deposited with the ATCC under accession number 98232;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BO538_2 deposited with the ATCC under accession number 98232;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BO538_2 deposited with the ATCC under accession number 98232;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BO538_2 deposited with the ATCC under accession number 98232;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:48;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:48;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:47.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:47 from nucleotide 45 to nucleotide 428; the nucleotide sequence of the full-length protein coding sequence of clone BO538_2 deposited with the ATCC under accession number 98232; or the nucleotide sequence of a mature protein coding sequence of clone BO538_2 deposited with the ATCC under accession number 98232. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BO538_2

(bd) the nucleotide sequence of the cDNA insert of clone BO432_4 deposited with the ATCC under accession number 98232;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:43, SEQ ID NO:44, and SEQ ID NO:46, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:43 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:46, but excluding the poly(A) tail at the 3' end of SEQ ID NO:46. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:44, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:44 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:44. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:44 from nucleotide 566 to nucleotide 631, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:44 from nucleotide 566 to nucleotide 631, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:44 from nucleotide 566 to nucleotide 631.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:45;

(b) a fragment of the amino acid sequence of SEQ ID NO:45, the fragment comprising eight contiguous amino acids of SEQ ID NO:45; and

(c) the amino acid sequence encoded by the cDNA insert of clone BO432_4 deposited with the ATCC under accession number 98232;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:45. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:45 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:45, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:45 having biological activity, the fragment comprising the amino acid sequence from amino acid 6 to amino acid 15 of SEQ ID NO:45.

ATCC under accession number 98232. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BO432_4 deposited with the ATCC under accession number 98232. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:45 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:45, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:45 having biological activity, the fragment comprising the amino acid sequence from amino acid 6 to amino acid 15 of SEQ ID NO:45.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:44, SEQ ID NO:43, and SEQ ID NO:46 . .

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:43;

(ab) SEQ ID NO:44;

(ac) SEQ ID NO:46, but excluding the poly(A) tail at the 3' end of SEQ ID NO:46; and

(ad) the nucleotide sequence of the cDNA insert of clone BO432_4 deposited with the ATCC under accession number 98232;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:43;

(bb) SEQ ID NO:44;

(bc) SEQ ID NO:46, but excluding the poly(A) tail at the 3' end of SEQ ID NO:46; and

fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising the amino acid sequence from amino acid 316 to amino acid 325 of SEQ ID NO:42.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:44;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:44 from nucleotide 566 to nucleotide 631;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BO432_4 deposited with the ATCC under accession number 98232;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BO432_4 deposited with the ATCC under accession number 98232;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BO432_4 deposited with the ATCC under accession number 98232;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BO432_4 deposited with the ATCC under accession number 98232;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:45;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:45 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:45;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:44.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:44 from nucleotide 566 to nucleotide 631; the nucleotide sequence of the full-length protein coding sequence of clone BO432_4 deposited with the ATCC under accession number 98232; or the nucleotide sequence of a mature protein coding sequence of clone BO432_4 deposited with the

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:41 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41 from nucleotide 102 to nucleotide 2027, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 102 to nucleotide 2027, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide 102 to nucleotide 2027. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41 from nucleotide 1902 to nucleotide 2027, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 1902 to nucleotide 2027, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide 1902 to nucleotide 2027. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41 from nucleotide 1 to nucleotide 431, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 1 to nucleotide 431, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide 1 to nucleotide 431.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:42;

(b) the amino acid sequence of SEQ ID NO:42 from amino acid 1 to amino acid 110;

(c) a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42; and

(d) the amino acid sequence encoded by the cDNA insert of clone BG160_1 deposited with the ATCC under accession number 98232;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:42 or the amino acid sequence of SEQ ID NO:42 from amino acid 1 to amino acid 110. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:42, or a protein comprising a

a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:42, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising the amino acid sequence from amino acid 316 to amino acid 325 of SEQ ID NO:42.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:41.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41; and

(ab) the nucleotide sequence of the cDNA insert of clone BG160_1 deposited with the ATCC under accession number 98232;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41; and

(bb) the nucleotide sequence of the cDNA insert of clone BG160_1 deposited with the ATCC under accession number 98232;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BG160_1 deposited with the ATCC under accession number 98232;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BG160_1 deposited with the ATCC under accession number 98232;

(g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BG160_1 deposited with the ATCC under accession number 98232;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BG160_1 deposited with the ATCC under accession number 98232;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:42;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:42;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:41.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:41 from nucleotide 102 to nucleotide 2027; the nucleotide sequence of SEQ ID NO:41 from nucleotide 1902 to nucleotide 2027; the nucleotide sequence of SEQ ID NO:41 from nucleotide 1 to nucleotide 431; the nucleotide sequence of the full-length protein coding sequence of clone BG160_1 deposited with the ATCC under accession number 98232; or the nucleotide sequence of a mature protein coding sequence of clone BG160_1 deposited with the ATCC under accession number 98232. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BG160_1 deposited with the ATCC under accession number 98232. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:42 from amino acid 1 to amino acid 110. In further preferred embodiments, the present invention provides

nucleotide 198 to nucleotide 2039. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39 from nucleotide 490 to nucleotide 809, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:39 from nucleotide 490 to nucleotide 809, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:39 from nucleotide 490 to nucleotide 809.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:40;

(b) the amino acid sequence of SEQ ID NO:40 from amino acid 106 to amino acid 204;

(c) a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40; and

(d) the amino acid sequence encoded by the cDNA insert of clone AY304_14 deposited with the ATCC under accession number 98561;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:40 or the amino acid sequence of SEQ ID NO:40 from amino acid 106 to amino acid 204. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:40, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising the amino acid sequence from amino acid 302 to amino acid 311 of SEQ ID NO:40.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41 from nucleotide 102 to nucleotide 2027;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41 from nucleotide 1902 to nucleotide 2027;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41 from nucleotide 1 to nucleotide 431;

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39; and

(ab) the nucleotide sequence of the cDNA insert of clone AY304_14 deposited with the ATCC under accession number 98561;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39; and

(bb) the nucleotide sequence of the cDNA insert of clone AY304_14 deposited with the ATCC under accession number 98561;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:39 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:39 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:39. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39 from nucleotide 198 to nucleotide 2039, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:39 from nucleotide 198 to nucleotide 2039, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:39 from

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AY304_14 deposited with the ATCC under accession number 98561;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:40;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:40;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:39.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:39 from nucleotide 198 to nucleotide 2039; the nucleotide sequence of SEQ ID NO:39 from nucleotide 490 to nucleotide 809; the nucleotide sequence of the full-length protein coding sequence of clone AY304_14 deposited with the ATCC under accession number 98561; or the nucleotide sequence of a mature protein coding sequence of clone AY304_14 deposited with the ATCC under accession number 98561. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AY304_14 deposited with the ATCC under accession number 98561. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:40 from amino acid 106 to amino acid 204. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:40, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising the amino acid sequence from amino acid 302 to amino acid 311 of SEQ ID NO:40.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:39.

376, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:36 from nucleotide 179 to nucleotide 376.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:37;

(b) the amino acid sequence of SEQ ID NO:37 from amino acid 1 to amino acid 91;

(c) a fragment of the amino acid sequence of SEQ ID NO:37, the fragment comprising eight contiguous amino acids of SEQ ID NO:37; and

(d) the amino acid sequence encoded by the cDNA insert of clone AS63_29 deposited with the ATCC under accession number 98232;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:37 or the amino acid sequence of SEQ ID NO:37 from amino acid 1 to amino acid 91. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:37 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:37, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:37 having biological activity, the fragment comprising the amino acid sequence from amino acid 48 to amino acid 57 of SEQ ID NO:37.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39 from nucleotide 198 to nucleotide 2039;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39 from nucleotide 490 to nucleotide 809;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AY304_14 deposited with the ATCC under accession number 98561;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AY304_14 deposited with the ATCC under accession number 98561;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AY304_14 deposited with the ATCC under accession number 98561;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:36;

(bb) SEQ ID NO:38, but excluding the poly(A) tail at the 3' end of SEQ ID NO:38; and

(bc) the nucleotide sequence of the cDNA insert of clone AS63_29 deposited with the ATCC under accession number 98232;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:36 and SEQ ID NO:38, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:36 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:38, but excluding the poly(A) tail at the 3' end of SEQ ID NO:38. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:36, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:36 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:36. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:36 from nucleotide 59 to nucleotide 376, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:36 from nucleotide 59 to nucleotide 376, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:36 from nucleotide 59 to nucleotide 376. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:36 from nucleotide 179 to nucleotide 376, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:36 from nucleotide 179 to nucleotide

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:36.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:36 from nucleotide 59 to nucleotide 376; the nucleotide sequence of SEQ ID NO:36 from nucleotide 179 to nucleotide 376; the nucleotide sequence of the full-length protein coding sequence of clone AS63_29 deposited with the ATCC under accession number 98232; or the nucleotide sequence of a mature protein coding sequence of clone AS63_29 deposited with the ATCC under accession number 98232. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AS63_29 deposited with the ATCC under accession number 98232. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:37 from amino acid 1 to amino acid 91. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:37 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:37, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:37 having biological activity, the fragment comprising the amino acid sequence from amino acid 48 to amino acid 57 of SEQ ID NO:37.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:36 and SEQ ID NO:38.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:36;

(ab) SEQ ID NO:38, but excluding the poly(A) tail at the 3' end of SEQ ID NO:38; and

(ac) the nucleotide sequence of the cDNA insert of clone AS63_29 deposited with the ATCC under accession number 98232;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:35 or the amino acid sequence of SEQ ID NO:35 from amino acid 51 to amino acid 221. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:35 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:35, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:35 having biological activity, the fragment comprising the amino acid sequence from amino acid 115 to amino acid 124 of SEQ ID NO:35.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:36;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:36 from nucleotide 59 to nucleotide 376;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:36 from nucleotide 179 to nucleotide 376;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AS63_29 deposited with the ATCC under accession number 98232;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AS63_29 deposited with the ATCC under accession number 98232;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AS63_29 deposited with the ATCC under accession number 98232;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AS63_29 deposited with the ATCC under accession number 98232;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:37;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:37 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:37;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(bb) the nucleotide sequence of the cDNA insert of clone AR415_4 deposited with the ATCC under accession number 98232;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:34, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:34 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:34 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:34. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:34 from nucleotide 437 to nucleotide 1159, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:34 from nucleotide 437 to nucleotide 1159, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:34 from nucleotide 437 to nucleotide 1159. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:34 from nucleotide 515 to nucleotide 1159, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:34 from nucleotide 515 to nucleotide 1159, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:34 from nucleotide 515 to nucleotide 1159. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:34 from nucleotide 539 to nucleotide 1099, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:34 from nucleotide 539 to nucleotide 1099, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:34 from nucleotide 539 to nucleotide 1099.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:35;

(b) the amino acid sequence of SEQ ID NO:35 from amino acid 51 to amino acid 221;

(c) a fragment of the amino acid sequence of SEQ ID NO:35, the fragment comprising eight contiguous amino acids of SEQ ID NO:35; and

(d) the amino acid sequence encoded by the cDNA insert of clone AR415_4 deposited with the ATCC under accession number 98232;

sequence of a mature protein coding sequence of clone AR415_4 deposited with the ATCC under accession number 98232. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AR415_4 deposited with the ATCC under accession number 98232. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:35 from amino acid 51 to amino acid 221. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:35 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:35, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:35 having biological activity, the fragment comprising the amino acid sequence from amino acid 115 to amino acid 124 of SEQ ID NO:35.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:34.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:34, but excluding the poly(A) tail at the 3' end of SEQ ID NO:34; and

(ab) the nucleotide sequence of the cDNA insert of clone AR415_4 deposited with the ATCC under accession number 98232;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:34, but excluding the poly(A) tail at the 3' end of SEQ ID NO:34; and

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:34 from nucleotide 437 to nucleotide 1159;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:34 from nucleotide 515 to nucleotide 1159;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:34 from nucleotide 539 to nucleotide 1099;

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AR415_4 deposited with the ATCC under accession number 98232;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AR415_4 deposited with the ATCC under accession number 98232;

(g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AR415_4 deposited with the ATCC under accession number 98232;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AR415_4 deposited with the ATCC under accession number 98232;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:35;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:35 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:35;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:34.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:34 from nucleotide 437 to nucleotide 1159; the nucleotide sequence of SEQ ID NO:34 from nucleotide 515 to nucleotide 1159; the nucleotide sequence of SEQ ID NO:34 from nucleotide 539 to nucleotide 1099; the nucleotide sequence of the full-length protein coding sequence of clone AR415_4 deposited with the ATCC under accession number 98232; or the nucleotide

from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:32 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:32, but excluding the poly(A) tail at the 3' end of SEQ ID NO:32. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:32 from nucleotide 338 to nucleotide 1198, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:32 from nucleotide 338 to nucleotide 1198, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:32 from nucleotide 338 to nucleotide 1198. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:32 from nucleotide 467 to nucleotide 1058, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:32 from nucleotide 467 to nucleotide 1058, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:32 from nucleotide 467 to nucleotide 1058.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:33;

(b) the amino acid sequence of SEQ ID NO:33 from amino acid 124 to amino acid 182;

(c) a fragment of the amino acid sequence of SEQ ID NO:33, the fragment comprising eight contiguous amino acids of SEQ ID NO:33; and

(d) the amino acid sequence encoded by the cDNA insert of clone DA136_11 deposited with the ATCC under accession number 98196;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:33 or the amino acid sequence of SEQ ID NO:33 from amino acid 124 to amino acid 182. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:33 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:33, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:33 having biological activity, the fragment comprising the amino acid sequence from amino acid 138 to amino acid 147 of SEQ ID NO:33.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:34;

fragment of the amino acid sequence of SEQ ID NO:33 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:33, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:33 having biological activity, the fragment comprising the amino acid sequence from amino acid 138 to amino acid 147 of SEQ ID NO:33.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:32.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:32, but excluding the poly(A) tail at the 3' end of SEQ ID NO:32; and

(ab) the nucleotide sequence of the cDNA insert of clone DA136_11 deposited with the ATCC under accession number 98196;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:32, but excluding the poly(A) tail at the 3' end of SEQ ID NO:32; and

(bb) the nucleotide sequence of the cDNA insert of clone DA136_11 deposited with the ATCC under accession number 98196;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:32, and extending contiguously

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone DA136_11 deposited with the ATCC under accession number 98196;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone DA136_11 deposited with the ATCC under accession number 98196;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone DA136_11 deposited with the ATCC under accession number 98196;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone DA136_11 deposited with the ATCC under accession number 98196;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:33;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:33 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:33;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:32.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:32 from nucleotide 338 to nucleotide 1198; the nucleotide sequence of SEQ ID NO:32 from nucleotide 467 to nucleotide 1058; the nucleotide sequence of the full-length protein coding sequence of clone DA136_11 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone DA136_11 deposited with the ATCC under accession number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone DA136_11 deposited with the ATCC under accession number 98196. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:33 from amino acid 124 to amino acid 182. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a

nucleotide 351, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:29 from nucleotide 28 to nucleotide 351, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:29 from nucleotide 28 to nucleotide 351. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29 from nucleotide 328 to nucleotide 351, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:29 from nucleotide 328 to nucleotide 351, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:29 from nucleotide 328 to nucleotide 351.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:30;

(b) the amino acid sequence of SEQ ID NO:30 from amino acid 56 to amino acid 108;

(c) a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30; and

(d) the amino acid sequence encoded by the cDNA insert of clone CC194_4 deposited with the ATCC under accession number 98196;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:30 or the amino acid sequence of SEQ ID NO:30 from amino acid 56 to amino acid 108. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:30, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising the amino acid sequence from amino acid 49 to amino acid 58 of SEQ ID NO:30.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:32;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:32 from nucleotide 338 to nucleotide 1198;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:32 from nucleotide 467 to nucleotide 1058;

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:29;

(ab) SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31; and

(ac) the nucleotide sequence of the cDNA insert of clone CC194_4 deposited with the ATCC under accession number 98196;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:29;

(bb) SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31; and

(bc) the nucleotide sequence of the cDNA insert of clone CC194_4 deposited with the ATCC under accession number 98196;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:29 and SEQ ID NO:31, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:29 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:29 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:29. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29 from nucleotide 28 to

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:30;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:29.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:29 from nucleotide 28 to nucleotide 351; the nucleotide sequence of SEQ ID NO:29 from nucleotide 328 to nucleotide 351; the nucleotide sequence of the full-length protein coding sequence of clone CC194_4 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone CC194_4 deposited with the ATCC under accession number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone CC194_4 deposited with the ATCC under accession number 98196. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:30 from amino acid 56 to amino acid 108. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:30, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising the amino acid sequence from amino acid 49 to amino acid 58 of SEQ ID NO:30.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:29 and SEQ ID NO:31.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(b) the amino acid sequence of SEQ ID NO:28 from amino acid 1 to amino acid 37;

(c) a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28; and

(d) the amino acid sequence encoded by the cDNA insert of clone BV141_2 deposited with the ATCC under accession number 98196;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:28 or the amino acid sequence of SEQ ID NO:28 from amino acid 1 to amino acid 37. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:28, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising the amino acid sequence from amino acid 33 to amino acid 42 of SEQ ID NO:28.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29 from nucleotide 28 to nucleotide 351;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29 from nucleotide 328 to nucleotide 351;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone CC194_4 deposited with the ATCC under accession number 98196;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone CC194_4 deposited with the ATCC under accession number 98196;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone CC194_4 deposited with the ATCC under accession number 98196;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone CC194_4 deposited with the ATCC under accession number 98196;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:30;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27; and

(bb) the nucleotide sequence of the cDNA insert of clone BV141_2 deposited with the ATCC under accession number 98196;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:27 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:27 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:27. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27 from nucleotide 101 to nucleotide 328, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:27 from nucleotide 101 to nucleotide 328, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:27 from nucleotide 101 to nucleotide 328. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27 from nucleotide 1 to nucleotide 197, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:27 from nucleotide 1 to nucleotide 197, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:27 from nucleotide 1 to nucleotide 197.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:28;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:27.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:27 from nucleotide 101 to nucleotide 328; the nucleotide sequence of SEQ ID NO:27 from nucleotide 1 to nucleotide 197; the nucleotide sequence of the full-length protein coding sequence of clone BV141_2 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone BV141_2 deposited with the ATCC under accession number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BV141_2 deposited with the ATCC under accession number 98196. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:28 from amino acid 1 to amino acid 37. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:28, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising the amino acid sequence from amino acid 33 to amino acid 42 of SEQ ID NO:28.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:27.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27; and

(ab) the nucleotide sequence of the cDNA insert of clone BV141_2 deposited with the ATCC under accession number 98196;

(d) the amino acid sequence encoded by the cDNA insert of clone BV140_3 deposited with the ATCC under accession number 98196;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:25 or the amino acid sequence of SEQ ID NO:25 from amino acid 29 to amino acid 57. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:25 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:25, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:25 having biological activity, the fragment comprising the amino acid sequence from amino acid 51 to amino acid 60 of SEQ ID NO:25.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27 from nucleotide 101 to nucleotide 328;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27 from nucleotide 1 to nucleotide 197;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BV141_2 deposited with the ATCC under accession number 98196;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BV141_2 deposited with the ATCC under accession number 98196;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BV141_2 deposited with the ATCC under accession number 98196;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BV141_2 deposited with the ATCC under accession number 98196;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:28;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:28;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:23;

(bb) SEQ ID NO:24;

(bc) SEQ ID NO:26, but excluding the poly(A) tail at the 3' end of SEQ ID NO:26; and

(bd) the nucleotide sequence of the cDNA insert of clone BV140_3 deposited with the ATCC under accession number 98196;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:23, SEQ ID NO:24, and SEQ ID NO:26, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:23 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:26, but excluding the poly(A) tail at the 3' end of SEQ ID NO:26. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:24, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:24 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:24. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:24 from nucleotide 57 to nucleotide 396, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:24 from nucleotide 57 to nucleotide 396, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:24 from nucleotide 57 to nucleotide 396.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:25;

(b) the amino acid sequence of SEQ ID NO:25 from amino acid 29 to amino acid 57;

(c) a fragment of the amino acid sequence of SEQ ID NO:25, the fragment comprising eight contiguous amino acids of SEQ ID NO:25; and

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:24 from nucleotide 57 to nucleotide 396; the nucleotide sequence of the full-length protein coding sequence of clone BV140_3 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone BV140_3 deposited with the ATCC under accession number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BV140_3 deposited with the ATCC under accession number 98196. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:25 from amino acid 29 to amino acid 57. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:25 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:25, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:25 having biological activity, the fragment comprising the amino acid sequence from amino acid 51 to amino acid 60 of SEQ ID NO:25.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:24, SEQ ID NO:23, and SEQ ID NO:26 .

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:23;

(ab) SEQ ID NO:24;

(ac) SEQ ID NO:26, but excluding the poly(A) tail at the 3' end of SEQ ID NO:26; and

(ad) the nucleotide sequence of the cDNA insert of clone BV140_3 deposited with the ATCC under accession number 98196;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:21 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:21, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:21 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:21.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:24;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:24 from nucleotide 57 to nucleotide 396;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BV140_3 deposited with the ATCC under accession number 98196;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BV140_3 deposited with the ATCC under accession number 98196;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BV140_3 deposited with the ATCC under accession number 98196;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BV140_3 deposited with the ATCC under accession number 98196;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:25;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:25 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:25;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:24.

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:20;

(bb) SEQ ID NO:22, but excluding the poly(A) tail at the 3' end of SEQ ID NO:22; and

(bc) the nucleotide sequence of the cDNA insert of clone BV51_1 deposited with the ATCC under accession number 98196;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:20 and SEQ ID NO:22, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:20 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:22, but excluding the poly(A) tail at the 3' end of SEQ ID NO:22. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:20, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:20 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:20. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:20 from nucleotide 68 to nucleotide 328, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:20 from nucleotide 68 to nucleotide 328, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:20 from nucleotide 68 to nucleotide 328.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:21;

(b) a fragment of the amino acid sequence of SEQ ID NO:21, the fragment comprising eight contiguous amino acids of SEQ ID NO:21; and

(c) the amino acid sequence encoded by the cDNA insert of clone BV51_1 deposited with the ATCC under accession number 98196;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:21. In further preferred embodiments, the

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:20.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:20 from nucleotide 68 to nucleotide 328; the nucleotide sequence of the full-length protein coding sequence of clone BV51_1 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone BV51_1 deposited with the ATCC under accession number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BV51_1 deposited with the ATCC under accession number 98196. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:21 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:21, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:21 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:21.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:20 and SEQ ID NO:22.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:20;

(ab) SEQ ID NO:22, but excluding the poly(A) tail at the 3' end of SEQ ID NO:22; and

(ac) the nucleotide sequence of the cDNA insert of clone BV51_1 deposited with the ATCC under accession number 98196;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:19. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:19 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:19, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:19 having biological activity, the fragment comprising the amino acid sequence from amino acid 113 to amino acid 122 of SEQ ID NO:19.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:20;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:20 from nucleotide 68 to nucleotide 328;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BV51_1 deposited with the ATCC under accession number 98196;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BV51_1 deposited with the ATCC under accession number 98196;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BV51_1 deposited with the ATCC under accession number 98196;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BV51_1 deposited with the ATCC under accession number 98196;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:21;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:21 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:21;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:18, but excluding the poly(A) tail at the 3' end of SEQ ID NO:18; and

(bb) the nucleotide sequence of the cDNA insert of clone BO365_2 deposited with the ATCC under accession number 98196;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:18, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:18 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:18 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:18. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:18 from nucleotide 1237 to nucleotide 1944, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:18 from nucleotide 1237 to nucleotide 1944, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:18 from nucleotide 1237 to nucleotide 1944. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:18 from nucleotide 737 to nucleotide 1072, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:18 from nucleotide 737 to nucleotide 1072, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:18 from nucleotide 737 to nucleotide 1072.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:19;

(b) a fragment of the amino acid sequence of SEQ ID NO:19, the fragment comprising eight contiguous amino acids of SEQ ID NO:19; and

(c) the amino acid sequence encoded by the cDNA insert of clone BO365_2 deposited with the ATCC under accession number 98196;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:18.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:18 from nucleotide 1237 to nucleotide 1944; the nucleotide sequence of SEQ ID NO:18 from nucleotide 737 to nucleotide 1072; the nucleotide sequence of the full-length protein coding sequence of clone BO365_2 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone BO365_2 deposited with the ATCC under accession number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BO365_2 deposited with the ATCC under accession number 98196. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:19 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:19, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:19 having biological activity, the fragment comprising the amino acid sequence from amino acid 113 to amino acid 122 of SEQ ID NO:19.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:18.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:18, but excluding the poly(A) tail at the 3' end of SEQ ID NO:18; and

(ab) the nucleotide sequence of the cDNA insert of clone BO365_2 deposited with the ATCC under accession number 98196;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(c) the amino acid sequence encoded by the cDNA insert of clone BO71_1 deposited with the ATCC under accession number 98196;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:16. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:16, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 8 to amino acid 17 of SEQ ID NO:16.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:18;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:18 from nucleotide 1237 to nucleotide 1944;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:18 from nucleotide 737 to nucleotide 1072;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BO365_2 deposited with the ATCC under accession number 98196;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BO365_2 deposited with the ATCC under accession number 98196;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BO365_2 deposited with the ATCC under accession number 98196;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BO365_2 deposited with the ATCC under accession number 98196;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:19;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:19 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:19;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:14;

(bb) SEQ ID NO:15;

(bc) SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17; and

(bd) the nucleotide sequence of the cDNA insert of clone BO71_1 deposited with the ATCC under accession number 98196;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:14, SEQ ID NO:15, and SEQ ID NO:17, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:14 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:15 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:15. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15 from nucleotide 459 to nucleotide 539, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:15 from nucleotide 459 to nucleotide 539, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:15 from nucleotide 459 to nucleotide 539.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:16;

(b) a fragment of the amino acid sequence of SEQ ID NO:16, the fragment comprising eight contiguous amino acids of SEQ ID NO:16; and

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:15.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:15 from nucleotide 459 to nucleotide 539; the nucleotide sequence of the full-length protein coding sequence of clone BO71_1 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone BO71_1 deposited with the ATCC under accession number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BO71_1 deposited with the ATCC under accession number 98196. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:16, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 8 to amino acid 17 of SEQ ID NO:16.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:15, SEQ ID NO:14, and SEQ ID NO:17 .

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:14;

(ab) SEQ ID NO:15;

(ac) SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17; and

(ad) the nucleotide sequence of the cDNA insert of clone BO71_1 deposited with the ATCC under accession number 98196;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

(d) the amino acid sequence encoded by the cDNA insert of clone BL249_18 deposited with the ATCC under accession number 98196;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:13 or the amino acid sequence of SEQ ID NO:13 from amino acid 3 to amino acid 102. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:13 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:13, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:13 having biological activity, the fragment comprising the amino acid sequence from amino acid 376 to amino acid 385 of SEQ ID NO:13.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 459 to nucleotide 539;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BO71_1 deposited with the ATCC under accession number 98196;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BO71_1 deposited with the ATCC under accession number 98196;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BO71_1 deposited with the ATCC under accession number 98196;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BO71_1 deposited with the ATCC under accession number 98196;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:16;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:16;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(ba) SEQ ID NO:12, but excluding the poly(A) tail at the 3' end of SEQ ID NO:12; and

(bb) the nucleotide sequence of the cDNA insert of clone BL249_18 deposited with the ATCC under accession number 98196;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:12, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:12 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:12 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:12. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:12 from nucleotide 2 to nucleotide 2290, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:12 from nucleotide 2 to nucleotide 2290, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:12 from nucleotide 2 to nucleotide 2290. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:12 from nucleotide 134 to nucleotide 2290, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:12 from nucleotide 134 to nucleotide 2290, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:12 from nucleotide 134 to nucleotide 2290. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:12 from nucleotide 1 to nucleotide 309, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:12 from nucleotide 1 to nucleotide 309, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:12 from nucleotide 1 to nucleotide 309.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:13;

(b) the amino acid sequence of SEQ ID NO:13 from amino acid 3 to amino acid 102;

(c) a fragment of the amino acid sequence of SEQ ID NO:13, the fragment comprising eight contiguous amino acids of SEQ ID NO:13; and

134 to nucleotide 2290; the nucleotide sequence of SEQ ID NO:12 from nucleotide 1 to nucleotide 309; the nucleotide sequence of the full-length protein coding sequence of clone BL249_18 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone BL249_18 deposited with the ATCC under accession number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BL249_18 deposited with the ATCC under accession number 98196. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:13 from amino acid 3 to amino acid 102. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:13 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:13, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:13 having biological activity, the fragment comprising the amino acid sequence from amino acid 376 to amino acid 385 of SEQ ID NO:13.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:12.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:12, but excluding the poly(A) tail at the 3' end of SEQ ID NO:12; and

(ab) the nucleotide sequence of the cDNA insert of clone BL249_18 deposited with the ATCC under accession number 98196;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:12;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:12 from nucleotide 2 to nucleotide 2290;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:12 from nucleotide 134 to nucleotide 2290;

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:12 from nucleotide 1 to nucleotide 309;

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BL249_18 deposited with the ATCC under accession number 98196;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BL249_18 deposited with the ATCC under accession number 98196;

(g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BL249_18 deposited with the ATCC under accession number 98196;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BL249_18 deposited with the ATCC under accession number 98196;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:13;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:13 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:13;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:12.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:12 from nucleotide 2 to nucleotide 2290; the nucleotide sequence of SEQ ID NO:12 from nucleotide

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:10, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:10 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:10, but excluding the poly(A) tail at the 3' end of SEQ ID NO:10. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:10 from nucleotide 302 to nucleotide 1762, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:10 from nucleotide 302 to nucleotide 1762, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:10 from nucleotide 302 to nucleotide 1762. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:10 from nucleotide 389 to nucleotide 1762, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:10 from nucleotide 389 to nucleotide 1762, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:10 from nucleotide 389 to nucleotide 1762. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:10 from nucleotide 1723 to nucleotide 2050, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:10 from nucleotide 1723 to nucleotide 2050, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:10 from nucleotide 1723 to nucleotide 2050.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:11;

(b) a fragment of the amino acid sequence of SEQ ID NO:11, the fragment comprising eight contiguous amino acids of SEQ ID NO:11; and

(c) the amino acid sequence encoded by the cDNA insert of clone BL187_4 deposited with the ATCC under accession number 98196;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:11. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:11 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:11, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:11 having biological activity, the fragment comprising the amino acid sequence from amino acid 238 to amino acid 247 of SEQ ID NO:11.

provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:11 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:11, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:11 having biological activity, the fragment comprising the amino acid sequence from amino acid 238 to amino acid 247 of SEQ ID NO:11.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:10.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:10, but excluding the poly(A) tail at the 3' end of SEQ ID NO:10; and

(ab) the nucleotide sequence of the cDNA insert of clone BL187_4 deposited with the ATCC under accession number 98196;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:10, but excluding the poly(A) tail at the 3' end of SEQ ID NO:10; and

(bb) the nucleotide sequence of the cDNA insert of clone BL187_4 deposited with the ATCC under accession number 98196;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

(d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:10 from nucleotide 1723 to nucleotide 2050;

(e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BL187_4 deposited with the ATCC under accession number 98196;

(f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BL187_4 deposited with the ATCC under accession number 98196;

(g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BL187_4 deposited with the ATCC under accession number 98196;

(h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BL187_4 deposited with the ATCC under accession number 98196;

(i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:11;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:11 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:11;

(k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

(n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:10.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:10 from nucleotide 302 to nucleotide 1762; the nucleotide sequence of SEQ ID NO:10 from nucleotide 389 to nucleotide 1762; the nucleotide sequence of SEQ ID NO:10 from nucleotide 1723 to nucleotide 2050; the nucleotide sequence of the full-length protein coding sequence of clone BL187_4 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone BL187_4 deposited with the ATCC under accession number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BL187_4 deposited with the ATCC under accession number 98196. In further preferred embodiments, the present invention

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:6, SEQ ID NO:7, and SEQ ID NO:9, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:6 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:7 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:7. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7 from nucleotide 206 to nucleotide 391, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:7 from nucleotide 206 to nucleotide 391, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:7 from nucleotide 206 to nucleotide 391.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:8;

(b) a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8; and

(c) the amino acid sequence encoded by the cDNA insert of clone BG241_1 deposited with the ATCC under accession number 98196;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:8. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:8, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 26 to amino acid 35 of SEQ ID NO:8.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:10;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:10 from nucleotide 302 to nucleotide 1762;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:10 from nucleotide 389 to nucleotide 1762;

sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 26 to amino acid 35 of SEQ ID NO:8.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:7, SEQ ID NO:6, and SEQ ID NO:9 .

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:6;

(ab) SEQ ID NO:7;

(ac) SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9; and

(ad) the nucleotide sequence of the cDNA insert of clone BG241_1 deposited with the ATCC under accession number 98196;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:6;

(bb) SEQ ID NO:7;

(bc) SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9; and

(bd) the nucleotide sequence of the cDNA insert of clone BG241_1 deposited with the ATCC under accession number 98196;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BG241_1 deposited with the ATCC under accession number 98196;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BG241_1 deposited with the ATCC under accession number 98196;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BG241_1 deposited with the ATCC under accession number 98196;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BG241_1 deposited with the ATCC under accession number 98196;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:8;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:8;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:7.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:7 from nucleotide 206 to nucleotide 391; the nucleotide sequence of the full-length protein coding sequence of clone BG241_1 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone BG241_1 deposited with the ATCC under accession number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BG241_1 deposited with the ATCC under accession number 98196. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:8, or a polynucleotide encoding a protein comprising a fragment of the amino acid

a nucleotide sequence corresponding to the 5' end of SEQ ID NO:4 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:4 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:4. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:4 from nucleotide 192 to nucleotide 2318, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:4 from nucleotide 192 to nucleotide 2318, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:4 from nucleotide 192 to nucleotide 2318. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:4 from nucleotide 653 to nucleotide 825, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:4 from nucleotide 653 to nucleotide 825, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:4 from nucleotide 653 to nucleotide 825.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:5;

(b) the amino acid sequence of SEQ ID NO:5 from amino acid 148 to amino acid 240;

(c) a fragment of the amino acid sequence of SEQ ID NO:5, the fragment comprising eight contiguous amino acids of SEQ ID NO:5; and

(d) the amino acid sequence encoded by the cDNA insert of clone BD335_14 deposited with the ATCC under accession number 98196;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:5 or the amino acid sequence of SEQ ID NO:5 from amino acid 148 to amino acid 240. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:5 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:5, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:5 having biological activity, the fragment comprising the amino acid sequence from amino acid 349 to amino acid 358 of SEQ ID NO:5.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 206 to nucleotide 391;

sequence of SEQ ID NO:5 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:5, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:5 having biological activity, the fragment comprising the amino acid sequence from amino acid 349 to amino acid 358 of SEQ ID NO:5.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:4.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:4, but excluding the poly(A) tail at the 3' end of SEQ ID NO:4; and

(ab) the nucleotide sequence of the cDNA insert of clone BD335_14 deposited with the ATCC under accession number 98196;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:4, but excluding the poly(A) tail at the 3' end of SEQ ID NO:4; and

(bb) the nucleotide sequence of the cDNA insert of clone BD335_14 deposited with the ATCC under accession number 98196;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:4, and extending contiguously from

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone BD335_14 deposited with the ATCC under accession number 98196;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone BD335_14 deposited with the ATCC under accession number 98196;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone BD335_14 deposited with the ATCC under accession number 98196;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone BD335_14 deposited with the ATCC under accession number 98196;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:5;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:5 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:5;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:4.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:4 from nucleotide 192 to nucleotide 2318; the nucleotide sequence of SEQ ID NO:4 from nucleotide 653 to nucleotide 825; the nucleotide sequence of the full-length protein coding sequence of clone BD335_14 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone BD335_14 deposited with the ATCC under accession number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone BD335_14 deposited with the ATCC under accession number 98196. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:5 from amino acid 148 to amino acid 240. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid

ID NO:1 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:1. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1 from nucleotide 282 to nucleotide 565, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:1 from nucleotide 282 to nucleotide 565, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:1 from nucleotide 282 to nucleotide 565. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1 from nucleotide 342 to nucleotide 565, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:1 from nucleotide 342 to nucleotide 565, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:1 from nucleotide 342 to nucleotide 565.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:2;

(b) a fragment of the amino acid sequence of SEQ ID NO:2, the fragment comprising eight contiguous amino acids of SEQ ID NO:2; and

(c) the amino acid sequence encoded by the cDNA insert of clone AX65_22 deposited with the ATCC under accession number 98196;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:2. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:2, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising the amino acid sequence from amino acid 42 to amino acid 51 of SEQ ID NO:2.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:4;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:4 from nucleotide 192 to nucleotide 2318;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:4 from nucleotide 653 to nucleotide 825;

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:1;

(ab) SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3; and

(ac) the nucleotide sequence of the cDNA insert of clone AX65_22 deposited with the ATCC under accession number 98196;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:1;

(bb) SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3; and

(bc) the nucleotide sequence of the cDNA insert of clone AX65_22 deposited with the ATCC under accession number 98196;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequences of SEQ ID NO:1 and SEQ ID NO:3, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:1 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone AX65_22 deposited with the ATCC under accession number 98196;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone AX65_22 deposited with the ATCC under accession number 98196;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:2;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:2;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:1.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:1 from nucleotide 282 to nucleotide 565; the nucleotide sequence of SEQ ID NO:1 from nucleotide 342 to nucleotide 565; the nucleotide sequence of the full-length protein coding sequence of clone AX65_22 deposited with the ATCC under accession number 98196; or the nucleotide sequence of a mature protein coding sequence of clone AX65_22 deposited with the ATCC under accession number 98196. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone AX65_22 deposited with the ATCC under accession number 98196. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:2, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising the amino acid sequence from amino acid 42 to amino acid 51 of SEQ ID NO:2.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:1 and SEQ ID NO:3.

SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

BACKGROUND OF THE INVENTION

Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization cloning techniques, have advanced the state of the art by making available large numbers of DNA/amino acid sequences for proteins that are known to have biological activity by virtue of their secreted nature in the case of leader sequence cloning, or by virtue of the cell or tissue source in the case of PCR-based techniques. It is to these proteins and the polynucleotides encoding them that the present invention is directed.

SUMMARY OF THE INVENTION

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 282 to nucleotide 565;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 342 to nucleotide 565;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone AX65_22 deposited with the ATCC under accession number 98196;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone AX65_22 deposited with the ATCC under accession number 98196;

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(57) Abstract: Novel polynucleotides and the proteins encoded thereby are disclosed.